

134

TTC GAC AAG CCC TAT CTG CTC GCG ATG GCC AAC GCC GGT CCG GGC ACC	866
Phe Asp Lys Pro Tyr Leu Leu Ala Met Ala Asn Ala Gly Pro Gly Thr	
100 105 110 115	
AAC GGC TCA CAG TTT TTC ATC ACC GTC GGC AAG ACT CCG CAC CTG AAC	614
Asn Gly Ser Gln Phe Phe Ile Thr Val Gly Lys Thr Pro His Leu Asn	
120 125 130	
CGG CGC CAC ACC ATT TTC GGT GAA GTG ATC GAC CCG GAG TCA CAG CGG	662
Arg Arg His Thr Ile Phe Gly Glu Val Ile Asp Ala Glu Ser Gln Arg	
135 140 145	
GTT GTG GAG GCG ATC TCC AAG ACG GCC ACC GAC GGC AAC GAT CGG CCG	710
Val Val Gln Ala Ile Ser Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro	
150 155 160	
ACG GAC CCG GTG GTG ATC GAG TCG ATC ACC ATC TCC TGA CCGGAAGCTA	759
Thr Asp Pro Val Val Ile Glu Ser Ile Thr Ile Ser	
165 170 175	
CGTGGGCTCG TCGCTCGAAT ACACCTTTGTG GACCCGCCAG GGCACGTGGC GGTACACCGA	819
CACGCCGTG GGGCCGTTCA ACCGACGCC CTCACGCCAA GTCGCTCAC CTTGGCCCGC	879
GACCGGCCGA ACCGGCAGCG GTAAGCGCAT CGAGCACCTC CACTGGGTCG GTGCCGAGAT	939
CCGACCGGGA	949

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Cys Asp Ser Val Thr Asn Ser Pro Leu Ala Thr Ala Thr	
-7 -5 1 5	
Ala Thr Leu His Thr Asn Arg Gly Asp Ile Lys Ile Ala Leu Phe Gly	
10 15 20 25	
Asn His Ala Pro Lys Thr Val Ala Asn Phe Val Gly Leu Ala Gln Gly	
30 35 40	
Thr Lys Asp Tyr Ser Thr Gln Asn Ala Ser Gly Gly Pro Ser Gly Pro	
45 50 55	
Phe Tyr Asp Gly Ala Val Phe His Arg Val Ile Gln Gly Phe Met Ile	
60 65 70	
Gln Gly Gly Asp Pro Thr Gly Thr Gly Arg Gly Gly Pro Gly Tyr Lys	
75 80 85	

135

Phe Ala Asp Glu Phe His Pro Glu Leu Gln Phe Asp Lys Pro Tyr Leu
 90 95 100 105
 Leu Ala Met Ala Asn Ala Gly Pro Gly Thr Asn Gly Ser Gln Phe Phe
 110 115 120
 Ile Thr Val Gly Lys Thr Pro His Leu Asn Arg Arg His Thr Ile Phe
 125 130 135
 Gly Glu Val Ile Asp Ala Glu Ser Gln Arg Val Val Glu Ala Ile Ser
 140 145 150
 Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro Thr Asp Pro Val Val Ile
 155 160 165
 Glu Ser Ile Thr Ile Ser
 170 175

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..860

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 201..296

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 297..860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGGACCTTCA CCGGCGGTCC CTTCGCTTCG GGCGCGACAC CTAACATACT GGTGTCACAC 50
 CTACCGCGAC ACCGCTGGGA CTTTGTGCCA TTCCCGGCCA CTCGGGSCCG CTGCGGCTTG 120
 GAAAAATTGG TCGGGCACGG GCGGCCCGGG GTCGCTACCA TCCACTGTG AATGATTTAC 180
 TGACCCGCCC ACTGCTCACC ATG GGC GCG GCC GCC GCA ATG CTG GCC GCG 230
 Met Gly Ala Ala Ala Ala Met Leu Ala Ala
 -32 -30 -25

136

GTG CTT CTG CTT ACT CCC ATC ACC GTT CCC GCC GGC TAC CCC GGT GCC	278
Val Leu Leu Leu Thr Pro Ile Thr Val Pro Ala Gly Tyr Pro Gly Ala	
-28 -15 -10	
GTT GCA CCG GCC ACT GCA GCC TGC CCC GAC GCC GAA GTG GTG TTC GCC	326
Val Ala Pro Ala Thr Ala Ala Cys Pro Asp Ala Glu Val Val Phe Ala	
-5 1 5 10	
CGC GGC CGC TTC GAA CCG CCC GGG ATT GGC ACG GTC GGC AAC GCA TTC	374
Arg Gly Arg Phe Glu Pro Pro Gly Ile Gly Thr Val Gly Asn Ala Phe	
15 20 25	
GTC AGC GCG CTG CCG TCG AAG GTC AAC AAG AAT GTC GGG GTC TAC GCG	422
Val Ser Ala Leu Arg Ser Lys Val Asn Lys Asn Val Gly Val Tyr Ala	
30 35 40	
GTG AAA TAC CCC GCC GAC AAT CAG ATC GAT GTG GGC CCC AAC GAC ATG	470
Val Lys Tyr Pro Ala Asp Asn Gln Ile Asp Val Gly Ala Asn Asp Met	
45 50 55	
AGC GCC CAC ATT CAG AGC ATG GCC AAC AGC TGT CCG AAT ACC CGC CTG	518
Ser Ala His Ile Gln Ser Met Ala Asn Ser Cys Pro Asn Thr Arg Leu	
60 65 70	
GTG CCC GGC GGT TAC TCG CTG GGC GCG GCC GTC ACC GAC GTG GTA CTC	566
Val Pro Gly Gly Tyr Ser Leu Gly Ala Ala Val Thr Asp Val Val Leu	
75 80 85 90	
GCG GTG CCC ACC CAG ATG TGG GGC TTC ACC AAT CCC CTG CCT CCC GGC	614
Ala Val Pro Thr Gln Met Trp Gly Phe Thr Asn Pro Leu Pro Pro Gly	
95 100 105	
ACT GAT GAG CAC ATC GCC GCG GTC GCG CTG TTC GGC AAT GGC AGT CAG	662
Ser Asp Glu His Ile Ala Ala Val Ala Leu Phe Gly Asn Gly Ser Gln	
110 115 120	
TGG GTC GGC CCC ATC ACC AAC TTC AGC CCC GCC TAC AAC GAT CCG ACC	710
Trp Val Gly Pro Ile Thr Asn Phe Ser Pro Ala Tyr Asn Asp Arg Thr	
125 130 135	
ATC GAG TTG TGT CAC GGC GAC GAC CCC GTC TGC CAC CCT GCC GAC CCC	758
Ile Glu Leu Cys His Gly Asp Asp Pro Val Cys His Pro Ala Asp Pro	
140 145 150	
AAC ACC TGG GAG GCC AAC TGG CCC CAG CAC CTC GCC GGG GCC TAT GTC	806
Asn Thr Trp Glu Ala Asn Trp Pro Gln His Leu Ala Gly Ala Tyr Val	
155 160 165 170	
TGG TGG GGC AAG GTC AAC CAG GCG GCT GAC TTC GTT GCC GGA AAG CTG	854
Ser Ser Gly Met Val Asn Gln Ala Ala Asp Phe Val Ala Gly Lys Leu	
175 180 185	
CAG TAG CCACCTAGCC CCGCGCGAG TCTTTGCTTC ACCCTTTCGC TAACCGACCA	910
Gln	
ACGCGCGCAC GATGGAGGGG TCCGTGGTCA TATCAAGACA AGAAGGGAGT AGCCGATGCA	970

137

CGCAAAAGTC GCGGACTACC TCGTGGTGAA GGGCACACCC ACCGACCGGC ATGATCAACA 1030
 TGCTGAGATC ATCGAGGTGC GCTCCGACAGA 1060

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Gly Ala Ala Ala Ala Met Leu Ala Ala Val Leu Leu Leu Thr Pro
 -32 -30 -25 -20
 Ile Thr Val Pro Ala Gly Tyr Pro Gly Ala Val Ala Pro Ala Thr Ala
 -15 -10 -5
 Ala Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Arg Phe Glu Pro
 1 5 10 15
 Pro Gly Ile Gly Thr Val Gly Asn Ala Phe Val Ser Ala Leu Arg Ser
 20 25 30
 Lys Val Asn Lys Asn Val Gly Val Tyr Ala Val Lys Tyr Pro Ala Asp
 35 40 45
 Asn Gln Ile Asp Val Gly Ala Asn Asp Met Ser Ala His Ile Gln Ser
 50 55 60
 Met Ala Asn Ser Cys Pro Asn Thr Arg Leu Val Pro Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Ala Val Thr Asp Val Val Leu Ala Val Pro Thr Gln Met
 85 90 95
 Trp Gly Phe Thr Asn Pro Leu Pro Pro Gly Ser Asp Glu His Ile Ala
 100 105 110
 Ala Val Ala Leu Phe Gly Asn Gly Ser Gln Trp Val Gly Pro Ile Thr
 115 120 125
 Asn Phe Ser Pro Ala Tyr Asn Asp Arg Thr Ile Glu Leu Cys His Gly
 130 135 140
 Asp Asp Pro Val Cys His Pro Ala Asp Pro Asn Thr Trp Glu Ala Asn
 145 150 155 160
 Trp Pro Gln His Leu Ala Gly Ala Tyr Val Ser Ser Gly Met Val Asn
 165 170 175
 Gln Ala Ala Asp Phe Val Ala Gly Lys Leu Gln
 180 185

(2) INFORMATION FOR SEQ ID NO: 15:

138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..998

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 201..998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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CAGATGCTGC GCAACATGTT TCTCGGCGAT CCGGCAGGCA ACACCGATCG AGTGCTTGAC      60
TTTTCCACCG CGGTGACCG CGGACTGTTT TTCTCACCCA CCATCGACTT TCTCGACCAT      120
CCACCGCCCC TACCGCAGGC GCGGACGCCA ACTCTGGCAG CCGGGTCGCT ATCGATCGGC      180
AGCTTGAAGG GAAGCCCCCG ATG AAC AAT CTC TAC CGC GAT TTS GCA CCG      230
          Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro
                1             5             10

GTC ACC GAA GCC GCT TGG GCG GAA ATC GAA TTG GAG GCG GCG CGG ACG      278
Val Thr Glu Ala Ala Trp Ala Glu Ile Glu Leu Glu Ala Ala Arg Thr
                15             20             25

TTC AAG CGA CAC ATC GCC GGG CGC CGG GTG GTC GAT GTC AGT GAT CCC      326
Phe Lys Arg His Ile Ala Gly Arg Arg Val Val Asp Val Ser Asp Pro
                30             35             40

GGG GGG CCC GTC ACC GCG GCG GTC AGC ACC GGC CGG CTG ATC GAT GTT      374
Gly Gly Pro Val Thr Ala Ala Val Ser Thr Gly Arg Leu Ile Asp Val
                45             50             55

AAG GCA CCA ACC AAC GGC GTG ATC GCC CAC CTG CGG GCC AGC AAA CCC      422
Lys Ala Pro Thr Asn Gly Val Ile Ala His Leu Arg Ala Ser Lys Pro
                60             65             70

CTT GTC CGG CTA CGG GTT CCG TTT ACC CTG TCG CGC AAC GAG ATC GAC      470
Leu Val Arg Leu Arg Val Pro Phe Thr Leu Ser Arg Asn Glu Ile Asp
                75             80             85             90

GAC GTG GAA CGT GGC TCT AAG GAC TCC GAT TGG GAA CCG GTA AAG GAG      518
Asp Val Glu Arg Gly Ser Lys Asp Ser Asp Trp Glu Pro Val Lys Glu
                95             100             105

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139

GGG GCC AAG AAG CTG GCC TTC GTC GAG GAC CGC ACA ATA TTC GAA GGC	566
Ala Ala Lys Lys Leu Ala Phe Val Glu Asp Arg Thr Ile Phe Glu Gly	
110 115 120	
TAC AGC GCC GCA TCA ATC GAA GGG ATC CGC AGC GCG AGT TCG AAC CCG	614
Tyr Ser Ala Ala Ser Ile Glu Gly Ile Arg Ser Ala Ser Ser Asn Pro	
125 130 135	
GGG CTG ACC TTG CCC GAG GAT CCC CGT GAA ATC CCT GAT GTC ATC TCC	662
Ala Leu Thr Leu Pro Glu Asp Pro Arg Glu Ile Pro Asp Val Ile Ser	
140 145 150	
CAG GCA TTG TCC GAA CTG CCG TTG GCC GGT GTG GAC GGA CCG TAT TCG	710
Gln Ala Leu Ser Glu Leu Arg Leu Ala Gly Val Asp Gly Pro Tyr Ser	
155 160 165 170	
GTG TTG CTC TCT GCT GAC GTC TAC ACC AAG GTT AGC GAG ACT TCC GAT	758
Val Leu Leu Ser Ala Asp Val Tyr Thr Lys Val Ser Glu Thr Ser Asp	
175 180 185	
CAC GGC TAT CCC ATC CGT GAG CAT CTG AAC CCG CTG GTG GAC GGG GAC	806
His Gly Tyr Pro Ile Arg Glu His Leu Asn Arg Leu Val Asp Gly Asp	
190 195 200	
ATC ATT TGG GCC CCG GCC ATC GAC GGC GCG TTC GTG CTG ACC ACT CGA	854
Ile Ile Trp Ala Pro Ala Ile Asp Gly Ala Phe Val Leu Thr Thr Arg	
205 210 215	
GGC GGC GAC TTC GAC CTA CAG CTG GGC ACC GAC GTT GCA ATC GGG TAC	902
Gly Gly Asp Phe Asp Leu Gln Leu Gly Thr Asp Val Ala Ile Gly Tyr	
220 225 230	
GGC AGC CAC GAC ACG GAC ACC GAG CGC CTC TAC CTG CAG GAG ACG CTG	950
Ala Ser His Asp Thr Asp Thr Glu Arg Leu Tyr Leu Gln Glu Thr Leu	
235 240 245 250	
ACG TTC CTT TSC TAC ACC GCC GAG GCG TCG GTC GCG CTC AGC CAC TAA	998
Thr Phe Leu Cys Tyr Thr Ala Glu Ala Ser Val Ala Leu Ser His	
255 260 265	
GGCAGGAGCG CGAGCAATAG CTCCTATGGC AAGCGGCCGC GGGTTGGGTG TGTTCGGAGC	1058
TGGGCTGGTG GACGGTGCSC AGGGCCTGGA AGACGGTGGC GGCTAGGCGG CTTTGGAGGC	1118
AGCGTAGTSC TGCGCGTTTG GTTTCCCGG CTTCTGCAG CCTTGGTAG TAGGCCTGGC	1178
CCCGGCTGTC GGTGATCCGG	1198

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

140

Met	Asn	Asn	Leu	Tyr	Arg	Asp	Leu	Ala	Pro	Val	Thr	Glu	Ala	Ala	Trp
1				5					10					15	
Ala	Glu	Ile	Glu	Leu	Glu	Ala	Ala	Arg	Thr	Phe	Lys	Arg	His	Ile	Ala
		20						25					30		
Gly	Arg	Arg	Val	Val	Asp	Val	Ser	Asp	Pro	Gly	Gly	Pro	Val	Thr	Ala
		35					40					45			
Ala	Val	Ser	Thr	Gly	Arg	Leu	Ile	Asp	Val	Lys	Ala	Pro	Thr	Asn	Gly
	50					55					60				
Val	Ile	Ala	His	Leu	Arg	Ala	Ser	Lys	Pro	Leu	Val	Arg	Leu	Arg	Val
65					70					75				80	
Pro	Phe	Thr	Leu	Ser	Arg	Asn	Glu	Ile	Asp	Asp	Val	Glu	Arg	Gly	Ser
				85					90					95	
Lys	Asp	Ser	Asp	Trp	Glu	Pro	Val	Lys	Glu	Ala	Ala	Lys	Lys	Leu	Ala
		100						105					110		
Phe	Val	Glu	Asp	Arg	Thr	Ile	Phe	Glu	Gly	Tyr	Ser	Ala	Ala	Ser	Ile
	115						120					125			
Glu	Gly	Ile	Arg	Ser	Ala	Ser	Ser	Asn	Pro	Ala	Leu	Thr	Leu	Pro	Glu
	130					135					140				
Asp	Pro	Arg	Glu	Ile	Pro	Asp	Val	Ile	Ser	Gln	Ala	Leu	Ser	Glu	Leu
145					150					155				160	
Arg	Leu	Ala	Gly	Val	Asp	Gly	Pro	Tyr	Ser	Val	Leu	Leu	Ser	Ala	Asp
			165					170						175	
Val	Tyr	Thr	Lys	Val	Ser	Glu	Thr	Ser	Asp	His	Gly	Tyr	Pro	Ile	Arg
	180							185					190		
Glu	His	Leu	Asn	Arg	Leu	Val	Asp	Gly	Asp	Ile	Ile	Trp	Ala	Pro	Ala
	195					200						205			
Ile	Asp	Gly	Ala	Phe	Val	Leu	Thr	Thr	Arg	Gly	Gly	Asp	Phe	Asp	Leu
	210					215					220				
Gln	Leu	Gly	Thr	Asp	Val	Ala	Ile	Gly	Tyr	Ala	Ser	His	Asp	Thr	Asp
225					230					235				240	
Thr	Glu	Arg	Leu	Tyr	Leu	Gln	Glu	Thr	Leu	Thr	Phe	Leu	Cys	Tyr	Thr
			245					250						255	
Ala	Glu	Ala	Ser	Val	Ala	Leu	Ser	His							
		260					265								

(3) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

141

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Ala is Ala or Ser

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 13
- (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala	Glu	Leu	Asp	Ala	Pro	Ala	Gln	Ala	Gly	Thr	Glu	Xaa	Ala	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ala	Gln	Ile	Thr	Leu	Arg	Gly	Asn	Ala	Ile	Asn	Thr	Val	Gly	Glu
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

142

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(ix) Feature:

- (A) NAME/KEY: Other
(B) LOCATION: 3
(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Asp	Pro	Xaa	Ser	Asp	Ile	Ala	Val	Val	Phe	Ala	Arg	Gly	Thr	His
1			S						10					15

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Thr	Asp	Ser	Pro	Leu	Ala	Thr	Ala	Thr	Ala	Thr	Leu	His	Thr	Asn
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(ix) Feature:

- (A) NAME/KEY: Other
(B) LOCATION: 3

143

(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Ala	Xaa	Pro	Asp	Ala	Glu	Val	Val	Phe	Ala	Arg	Gly	Arg	Phe	Glu
1				5						10				15

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 1
- (C) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Ile is Ile or Val

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Val is Val or Thr

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 11
- (D) OTHER INFORMATION: Val is Val or Phe

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 14
- (D) OTHER INFORMATION: Asp is Asp or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Xaa	Ile	Gln	Lys	Ser	Leu	Glu	Leu	Ile	Val	Val	Thr	Ala	Asp	Glu
1					5					10				15

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

344

(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(iv) **FRAGMENT TYPE:** N-terminal

(vii) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro Val Thr Glu Ala Ala Trp
2 3 15 18

Ma Ga Ne

(2) INFORMATION FOR GEO ID NO. 24:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCGGCTGGA GAACCTGTAC CCGGACCTGG CAGC

203

(2) INFORMATION FOR DND ID NO: 25:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(//) MOLECULE TYPE: DNA (synthetic)

(41) SECURITY DESCRIPTION: STD ID NO: 25.

GGGCGCGATC CGAGCGCGCG TCGTTCACCG GTTCCG

22

(2) INFORMATION FOR SRC ID NO: 26:

145

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGAAGCCCCA TATGAACAT CTCTACCG

28

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CGCGCTCAGC CCTTAGTGAC TGAGCCCGAC CG

32

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CTCGAATTCC CCGGCTGCAC ACAG

24

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

146

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTOGAATTGG CCCCCATACG AGAAC

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GTGTATCTGC TGGAC

15

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCGACTGCTT GCGCG

15

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

147

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGGAAATTCG CTTAGCGGAT CGCA

24

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCACATTCG GTTGG

15

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GTCCAGCAGA TACAC

15

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GTACGAGAAT TCATGTGCGA ATTCATG

27

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTACGAGAAT TCGAGCTTGG GGTGCCG

27

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CGATTCCAAAG CTTGTGGCCG CCGACCCG

28

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGTTAGGGAT CCTCATCGCC ATGGTGTGTTGG

30

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CGTTAGGGAT CCGGTTCCAC TGTGCC

26

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGTTAGGGAT CCTCAGGTCT TTCCGATG

28

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

150

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 45..944

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..143

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 144..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAATTCGCCG GGTGCACACA GCCTTACACG ACGGAGGTGG ACAC ATG AAG GGT CCG	56
Met Lys Gly Arg	
-33 -30	
TCG GCG CTG CTG CCG GCG CTC TGG ATT GCC GCA CTG TCA TTC GGG TTG	104
Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu Ser Phe Gly Leu	
-25 -20 -15	
GGC GGT GTC GCG GTA GCC GCG GAA CCC ACC GCC AAG GGC GCC CCA TAC	152
Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys Ala Ala Pro Tyr	
-10 -5 1	
GAG AAC CTG ATG GTG CCG TCG CCC TCG ATG GGC CCG GAC ATC CCG GTG	200
Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg Asp Ile Pro Val	
5 10 15	
GCC TTC CTA GCC GGT GGG CCG CAC GCG GTG TAT CTG CTG GAC GCC TTC	248
Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu Leu Asp Ala Phe	
20 25 30 35	
AAC GCC GGC CCG GAT GTC AGT AAC TGG GTC ACC GCG GGT AAC GCG ATG	296
Asn Ala Gly Pro Asp Val Ser Asn Trp Val Thr Ala Gly Asn Ala Met	
40 45 50	
AAC ACG TTG GCG GGC AAG GGG ATT TCG GTG GTG GCA CCG GCC GGT GGT	344
Asn Thr Leu Ala Gly Lys Gly Ile Ser Val Val Ala Pro Ala Gly Gly	
55 60 65	
GCG TAC AGC ATG TAC ACC AAC TGG GAG CAG GAT GGC AGC AAG CAG TGG	392
Ala Tyr Ser Met Tyr Thr Asn Trp Glu Gln Asp Gly Ser Lys Gln Trp	
70 75 80	
GAC ACC TTC TTG TCC GCT GAG CTG CCC GAC TGG CTG GCC GCT AAC CCG	440
Asp Thr Phe Leu Ser Ala Glu Leu Pro Asp Trp Leu Ala Ala Asn Arg	
85 90 95	
GGC TTG GCC CCC GGT GGC CAT GCG GCC GTT GGC GCC GCT CAG GGC GGT	488
Gly Leu Ala Pro Gly Gly His Ala Ala Val Gly Ala Ala Gln Gly Gly	
100 105 110 115	
TAC GGG GCG ATG GCG CTG GCG GCC TTC CAC CCC GAC CCG TTC GGC TTC	536
Tyr Gly Ala Met Ala Leu Ala Ala Phe His Pro Asp Arg Phe Gly Phe	
120 125 130	

151

GCT GGC TGG ATG TCG GGC TTT TTG TAC CCG TCG AAC ACC ACC ACC AAC	584
Ala Gly Ser Met Ser Gly Phe Leu Tyr Pro Ser Asn Thr Thr Thr Asn	
135 140 145	
GGT GCG ATC GCG GCG GGC ATG CAG CAA TTC GGC GGT GTG GAC ACC AAC	632
Gly Ala Ile Ala Ala Gly Met Gln Gln Phe Gly Gly Val Asp Thr Asn	
150 155 160	
GGA ATG TGG GGA GCA CCA CAG CTG GGT CCG TGG AAG TGG CAC GAC CCG	680
Gly Met Trp Gly Ala Pro Gln Leu Gly Arg Trp Lys Trp His Asp Pro	
165 170 175	
TGG GTG CAT GCC AGC CTG CTG GCG CAA AAC AAC ACC CCG GTG TGG GTG	728
Trp Val His Ala Ser Leu Leu Ala Gln Asn Asn Thr Arg Val Trp Val	
180 185 190 195	
TGG AGC CCG ACC AAC CCG GGA GGC AGC GAT CCC GCC GGC ATG ATC GGC	776
Trp Ser Pro Thr Asn Pro Gly Ala Ser Asp Pro Ala Ala Met Ile Gly	
200 205 210	
CAA ACC GCC GAG GCG ATG GGT AAC AGC CGC ATG TTC TAC AAC CAG TAT	824
Gln Thr Ala Glu Ala Met Gly Asn Ser Arg Met Phe Tyr Asn Gln Tyr	
215 220 225	
CGC AGC GTC GGC GGG CAC AAC GGA CAC TTC GAC TTC CCA GCC AGC GGT	872
Arg Ser Val Gly Gly His Asn Gly His Phe Asp Phe Pro Ala Ser Gly	
230 235 240	
GAC AAC GGC TGG GGC TCG TGG GCG CCC CAG CTG GGC GCT ATG TCG GGC	920
Asp Asn Gly Trp Gly Ser Trp Ala Pro Gln Leu Gly Ala Met Ser Gly	
245 250 255	
GAT ATC GTC GGT GCG ATC CCG TAA GCGAATTC	952
Asp Ile Val Gly Ala Ile Arg	
260 265	

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Gly Arg Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu	
-33 -30 -25 -20	
Ser Phe Gly Leu Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys	
-15 -10 -5	
Ala Ala Pro Tyr Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg	
1 5 10 15	
Asp Ile Pro Val Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu	
20 25 30	

152

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Leu Asp Ala Phe Asn Ala Gly Pro Asp Val Ser Asn Trp Val Thr Ala
    35                                40                                45

Gly Asn Ala Met Asn Thr Leu Ala Gly Lys Gly Ile Ser Val Val Ala
    50                                55                                60

Pro Ala Gly Gly Ala Tyr Ser Met Tyr Thr Asn Trp Glu Gln Asp Gly
    65                                70                                75

Ser Lys Gln Trp Asp Thr Phe Leu Ser Ala Glu Leu Pro Asp Trp Leu
    80                                85                                90                                95

Ala Ala Asn Arg Gly Leu Ala Pro Gly Gly His Ala Ala Val Gly Ala
    100                               105                               110

Ala Gln Gly Gly Tyr Gly Ala Met Ala Leu Ala Ala Phe His Pro Asp
    115                               120                               125

Arg Phe Gly Phe Ala Gly Ser Met Ser Gly Phe Leu Tyr Pro Ser Asn
    130                               135                               140

Thr Thr Thr Asn Gly Ala Ile Ala Ala Gly Met Gln Gln Phe Gly Gly
    145                               150                               155

Val Asp Thr Asn Gly Met Trp Gly Ala Pro Gln Leu Gly Arg Trp Lys
    160                               165                               170                               175

Trp His Asp Pro Trp Val His Ala Ser Leu Leu Ala Gln Asn Asn Thr
    180                               185                               190

Arg Val Trp Val Trp Ser Pro Thr Asn Pro Gly Ala Ser Asp Pro Ala
    195                               200                               205

Ala Met Ile Gly Gln Thr Ala Glu Ala Met Gly Asn Ser Arg Met Phe
    210                               215                               220

Tyr Asn Gln Tyr Arg Ser Val Gly Gly His Asn Gly His Phe Asp Phe
    225                               230                               235

Pro Ala Ser Gly Asp Asn Gly Trp Gly Ser Trp Ala Pro Gln Leu Gly
    240                               245                               250                               255

Ala Met Ser Gly Asp Ile Val Gly Ala Ile Arg
    260                               265

```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GCAACACCCCG GGAATGTCGCA AATCATG

27

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTAACACCCCG GGGTGGCCCGC CGACCCG

27

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CTACTAAGCT TGGATCCCTA GCCGCCCCAT TTGGCGG

37

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CTACTAAGCT TCCATGGTCA GGTCTTTTCG ATGCTTAC

38

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 105...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTGCGCGCGCT CCCAGGGTT CTTATGGTTC GATATACCTG AGTTTGATGG AAGTCCGATG 60

ACCAGCAGTC AGCATAACGGC ATGGCCGAAA AGAGTGGGGT GATG ATG GCC GAG GAT 116
Met Ala Glu Asp
1

GTT CGC GCC GAG ATC GTG GCC AGC GTT CTC GAA GTC GTT GTC AAC GAA 164
Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val Val Asn Glu
5 10 15 20

GGC GAT CAG ATC GAC AAG GGC GAC GTC GTG GTG CTG CTG GAG TCG ATG 212
Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu Glu Ser Met
25 30 35

AAG ATG GAG ATC CCC GTC CTG GCC GAA GCT GCC GGA ACG GTC ACC AAG 260
Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr Val Ser Lys
40 45 50

GTG GCG GTA TCG GTG GGC GAT GTC ATT CAG GCC GGC GAC CTT ATC GCG 308
Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly Asp Leu Ile Ala
55 60 65

GTG ATC ACC TAGTCGTTGA TAGTCACTCA TGTCACACT CGGTGATCTG CTCGCCGAA 366
Val Ile Ser
70

CACACGGTGC TGCCGGGCAG CCGGGTGGAC CACCTGCATG CCGTGGTCCG GGAATGGCAG 426

CTCCTTGCCG ACTTGTCGTT TGCC 450

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

155

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

Met Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val
 1           5           10           15
Val Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu
          20           25           30
Leu Glu Ser Met Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly
          35           40           45
Thr Val Ser Lys Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly
          50           55           60
Asp Leu Ile Ala Val Ile Ser
65           70

```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 113...640

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

GGGTACCCAT CGATGGGTTG CGGTTCCGCA CCGAGGTGCT AACGCACTTG CTGACACACT      60
GCTAGTCGAA AACGAGGCTA GTCCCAACGT CGATCACACG AGAGGACTGA CC ATG ACA      118
                                     Met Thr
                                     1
ACT TCA CCC GAC CCG TAT GCC GCG CTG CCC AAG CTG CCG TCC TTC AGC      166
Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser Phe Ser
          5           10           15
CTG ACG TCA ACC TCG ATC ACC GAT GGG CAG CCG CTG GCT ACA CCC CAG      214
Leu Thr Ser Thr Ser Ile Thr Asp Gly Gln Pro Leu Ala Thr Pro Gln
          20           25           30
GTC ACC GGG ATC ATG GGT GCG GGC GGG GCG GAT GCC AGT CCG CAG CTG      262
Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro Gln Leu
          35           40           45           50

```

156

AGG TGG TCG GGA TTT CCC AGC GAG ACC CGC AGC TTC GCG GTA ACC GTC	310
Arg Trp Ser Gly Phe Pro Ser Glu Thr Arg Ser Phe Ala Val Thr Val	
55 60 65	
TAC GAC CCT GAT GCC CCC ACC CTG TCC GGG TTC TGG CAC TGG GCG GTG	358
Tyr Asp Pro Asp Ala Pro Thr Leu Ser Gly Phe Trp His Trp Ala Val	
70 75 80	
GCC AAC CTG CCT GCC AAC GTC ACC GAG TTG CCC GAG GGT GTC GGC GAT	406
Ala Asn Leu Pro Ala Asn Val Thr Glu Leu Pro Glu Gly Val Gly Asp	
85 90 95	
GGC CGC GAA CTG CCG GGC GGG GCA CTG ACA TTG GTC AAC GAC GCC GGT	454
Gly Arg Glu Leu Pro Gly Gly Ala Leu Thr Leu Val Asn Asp Ala Gly	
100 105 110	
ATG CGC CCG TAT GTG GGT GCG GCG CCG CCT CCC GGT CAT GGG GTG CAT	502
Met Arg Arg Tyr Val Gly Ala Ala Pro Pro Pro Gly His Gly Val His	
115 120 125 130	
CGC TAC TAC GTC GCG GTA CAC GCG GTG AAG GTC GAA AAG CTC GAC CTC	550
Arg Tyr Tyr Val Ala Val His Ala Val Lys Val Glu Lys Leu Asp Leu	
135 140 145	
CCC GAG GAC GCG AGT CCT GCA TAT CTG GGA TTC AAC CTG TTC CAG CAC	598
Pro Glu Asp Ala Ser Pro Ala Tyr Leu Gly Phe Asn Leu Phe Gln His	
150 155 160	
GCG AAT GCA CGA GCG GTC ATC TTC GGC ACC TAC GAG CAG CGT TAGCGCTTT	649
Ala Ile Ala Arg Ala Val Ile Phe Gly Thr Tyr Glu Gln Arg	
165 170 175	
AGCTGGGTTG CCGACGTCTT GCGGAGCCGA CCGCTTCGTG CAGCGAGCCG AACCCGCCGT	709
CATGCAGCCT GCGGGCAATG CCTTCATGGA TGTCCTTGGC C	750

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Thr Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser	
1 5 10 15	
Phe Ser Leu Thr Ser Thr Ser Ile Thr Asp Gly Gln Pro Leu Ala Thr	
20 25 30	
Pro Gln Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro	
35 40 45	

157

Gln Leu Arg Trp Ser Gly Phe Pro Ser Glu Thr Arg Ser Phe Ala Val
 50 55 60
 Thr Val Tyr Asp Pro Asp Ala Pro Thr Leu Ser Gly Phe Trp His Trp
 65 70 75 80
 Ala Val Ala Asn Leu Pro Ala Asn Val Thr Glu Leu Pro Glu Gly Val
 85 90 95
 Gly Asp Gly Arg Glu Leu Pro Gly Gly Ala Leu Thr Leu Val Asn Asp
 100 105 110
 Ala Gly Met Arg Arg Tyr Val Gly Ala Ala Pro Pro Pro Gly His Gly
 115 120 125
 Val His Arg Tyr Tyr Val Ala Val His Ala Val Lys Val Glu Lys Leu
 130 135 140
 Asp Leu Pro Glu Asp Ala Ser Pro Ala Tyr Leu Gly Phe Asn Leu Phe
 145 150 155 160
 Gln His Ala Ile Ala Arg Ala Val Ile Phe Gly Thr Tyr Glu Gln Arg
 165 170 175

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...695
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 18...134
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TCATGAGGTT CATCGGG GTG ATC CCA CGC CCG CAG CCG CAT TCG GGC CGC 50
 Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg
 -35 -30
 TGG CGA GCC GGT GCC GCA CGC CGC CTC ACC AGC CTG GTG GCC GCC GCC 55
 Trp Arg Ala Gly Ala Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala
 -35 -20 -15
 TTT GCG GCG GCC ACA CTG TTG CTT ACC CCC GCG CTG GCA CCA CCG GCA 146
 Phe Ala Ala Ala Thr Leu Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala
 -10 -5 1 5

158

TCG GCG GGC TGC CCG GAT GCC GAG GTG GTG TTC GCC CGC GGA ACC GGC	194
Ser Ala Gly Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly	
10 15 20	
GAA CCA CCT GGC CTC GGT CGG GTA GGC CAA GCT TTC GTC AGT TCA TTG	242
Glu Pro Pro Gly Leu Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu	
25 30 35	
CGC CAG CAG ACC AAC AAG AGC ATC GGG ACA TAC GGA GTC AAC TAC CCG	290
Arg Gln Gln Thr Asn Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro	
40 45 50	
GCC AAC GGT GAT TTC TTG GCC GCC GCT GAC GGC GCG AAC GAC GCC AGC	338
Ala Asn Gly Asp Phe Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser	
55 60 65	
GAC CAC ATT CAG CAG ATG GCC AGC GCG TGC CGG GCC ACG AGG TTG GTG	386
Asp His Ile Gln Gln Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val	
70 75 80 85	
CTC GGC GGC TAC TCC CAG GGT GCG GCC GTG ATC GAC ATC GTC ACC GCC	434
Leu Gly Gly Tyr Ser Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala	
90 95 100	
GCA CCA CTG CCC GGC CTC GGG TTC ACG CAG CCG TTG CCG CCC GCA GCG	482
Ala Pro Leu Pro Gly Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala	
105 110 115	
GAC GAT CAC ATC GCC GCG ATC GCC CTG TTC GGG AAT CCC TCG GGC CGC	530
Asp Asp His Ile Ala Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg	
120 125 130	
GCT GGC GGG CTG ATG ACC GCC CTG ACC CCT CAA TTC GGG TCC AAG ACC	578
Ala Gly Gly Leu Met Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr	
135 140 145	
ATC AAC CTC TGC AAC AAC GGC GAC CCG ATT TGT TCG GAC GGC AAC CGG	626
Ile Asn Leu Cys Asn Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg	
150 155 160 165	
TGG CGA GCG CAC CTA GGC TAC GTG CCC GGG ATG ACC AAC CAG GCG GCG	674
Trp Arg Ala His Leu Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala	
170 175 180	
CGT TTC GTC GCG AGC AGG ATC TAACGCGAGC CGCCCCATAG ATTCCGGCTA AGCA	722
Arg Phe Val Ala Ser Arg Ile	
185	
ACGGCTGCGC CGCCGCCCGG CCACBAGTGA CCGCCGCCGA CTGGCACACC GCTTACCAGC	789
GCCPTATGCT G	800

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

159

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(vi) FRAGMENT TYPE: internal
(ix) FEATURE:

(A) NAME/KEY: Signal Sequence
(B) LOCATION: 1...38
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg Trp Arg Ala Gly Ala
      -35                      -30                      -25

Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala Phe Ala Ala Ala Thr
      -20                      -15                      -10

Leu Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala Ser Ala Gly Cys Pro
      -5                      1                      5                      10

Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Leu
      15                      20                      25

Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu Arg Gln Gln Thr Asn
      30                      35                      40

Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro Ala Asn Gly Asp Phe
      45                      50                      55

Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser Asp His Ile Gln Gln
      60                      65                      70

Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val Leu Gly Gly Tyr Ser
      75                      80                      85                      90

Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala Ala Pro Leu Pro Gly
      95                      100                      105

Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala Asp Asp His Ile Ala
      110                      115                      120

Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg Ala Gly Gly Leu Met
      125                      130                      135

Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr Ile Asn Leu Cys Asn
      140                      145                      150

Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg Trp Arg Ala His Leu
      155                      160                      165                      170

Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala Arg Phe Val Ala Ser
      175                      180                      185

Arg Ile

```

160

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...615
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

CTAGGAAGAGC CTTTCCTGAG TAAGTATTGC CTTTCGTTGCA TAACCCCTTT TACCTGCCTT      60
AATCTGCATT TT ATG ACA GAA TAC GAA GGG CCT AAG ACA AAA TTC CAC GCG      111
      Met Thr Glu Tyr Glu Gly Pro Lys Thr Lys Phe His Ala
              1              5              10

TTA ATG CAG GAA CAG ATT CAT AAC GAA TTC ACA GCG GCA CAA CAA TAT      153
Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr Ala Ala Gln Gln Tyr
      15              20              25

GTC GCG ATC GCG GTT TAT TTC GAC AGC GAA GAC CTG CCG CAG TTG GCG      207
Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp Leu Pro Gln Leu Ala
      30              35              40              45

ARG CAT TTT TAC AGC CAA GCG GTC GAG GAA CGA AAC CAT GCA ATG ATG      255
Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg Asn His Ala Met Met
              50              55              60

CTC GTG CAA CAC CTG CTC GAC CGC GAC CTT CGT GTC GAA ATT CCC GGC      303
Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg Val Glu Ile Pro Gly
              65              70              75

GTA GAC ACC GTG CGA AAC CAG TTC GAC AGA CCC CGC GAG GCA CTG GCG      351
Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro Arg Glu Ala Leu Ala
              80              85              90

CTG GCG CTC GAT CAG GAA CGC ACA GTC ACC GAC CAG GTC GGT CGG CTG      399
Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp Gln Val Gly Arg Leu
              95              100              105

ACA GCG GTG GCC CGC GAC GAG GGC GAT TTC CTC GGC GAG CAG TTC ATG      447
Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln Phe Met
      110              115              120              125

CAG TGG TTC TTG CAG GAA CAG ATC GAA GAG GTG GCC TTG ATG GCA ACC      495
Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val Ala Leu Met Ala Thr
              130              135              140

CTG GTG CCG GTT GCC GAT CGG GCG GCG GCC AAC CTG TTC GAG CTA GAG      543
Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn Leu Phe Glu Leu Glu
              145              150              155

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161

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AAC TTC GTC GCA CCG GAA GTG GAT GTG GCG CCG GCC GCA TCA GGC GCC      591
Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro Ala Ala Ser Gly Ala
      160              165              170

CCG CAC GCT GCC GGG GGC CGC CTC TAGATCCCTG GCGGGGATCA GCGAGTGGTC      645
Pro His Ala Ala Gly Gly Arg Leu
      175              180

CCGTTCCGCC GCGGCTCTTC CAGCCAGGCC TTGGTGCGGC CCGGCTGGTG AGTAC      700

```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

Met Thr Glu Tyr Glu Gly Pro Lys Thr Lys Phe His Ala Leu Met Gln
 1              5              10              15

Glu Gln Ile His Asn Glu Phe Thr Ala Ala Gln Gln Tyr Val Ala Ile
      20              25              30

Ala Val Tyr Phe Asp Ser Glu Asp Leu Pro Gln Leu Ala Lys His Phe
      35              40              45

Tyr Ser Gln Ala Val Glu Glu Arg Asn His Ala Met Met Leu Val Gln
      50              55              60

His Leu Leu Asp Arg Asp Leu Arg Val Glu Ile Pro Gly Val Asp Thr
      65              70              75              80

Val Arg Asn Gln Phe Asp Arg Pro Arg Glu Ala Leu Ala Leu Ala Leu
      85              90              95

Asp Gln Glu Arg Thr Val Thr Asp Gln Val Gly Arg Leu Thr Ala Val
      100              105              110

Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln Phe Met Gln Trp Phe
      115              120              125

Leu Gln Glu Gln Ile Glu Glu Val Ala Leu Met Ala Thr Leu Val Arg
      130              135              140

Val Ala Asp Arg Ala Gly Ala Asn Leu Phe Glu Leu Glu Asn Phe Val
      145              150              155              160

Ala Arg Glu Val Asp Val Ala Pro Ala Ala Ser Gly Ala Pro His Ala
      165              170              175

```

162

Ala Gly Gly Arg Leu
180

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 133...918
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 133...233
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TGGGCTCGGC ACTGGCTCTC CCACGGTGGC GCGCTGATTT CTCCCCACGG TAGGCSTTGC	60
GACGCATGTT CTTCACCGTC TATCCACAGC TACCGACATT TGCTCCGGCT GGATCGCGGG	120
TAAATTCCG TC GTG AAC AAT CGA CCC ATC CGC CTG CTG ACA TCC GGC AGG	171
Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg	
-30 -25	
GCT GGT TTG GGT GCG GGC GCA TTG ATC ACC GCC GTC GTC CTG CTC ATC	219
Ala Gly Leu Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile	
-20 -15 -10 -5	
GCC TTG GGC GCT GTT TGG ACC CCG GTT GCC TTC GCC GAT GGA TGC CCG	267
Ala Leu Gly Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro	
1 5 10	
GAC GCC GAA GTC ACG TTC GCC CGC GGC ACC GGC GAG CCG CCC GGA ATC	315
Asp Ala Glu Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile	
15 20 25	
GGG CGC GTT GGC CAG GCG TTC GTC GAC TCG CTG CGC CAG CAG ACT GGC	363
Gly Arg Val Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly	
30 35 40	
ATG GAG ATC GGA GTA TAC CCG GTG AAT TAC GCC GCC AGC CGC CTA CAG	411
Met Glu Ile Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Gln	
45 50 55 60	
CTG CAC GGG GGA GAC GGC GCC AAC GAC GCC ATA TCG CAC ATT AAG TCC	459
Leu His Gly Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser	
65 70 75	

163

ATG GGC TCG TCA TGC CCG AAC ACC AAG CTG GTC TTG GGC GGC TAT TCG	507
Met Ala Ser Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser	
80 85 90	
CAG GGC GCA ACC GTG ATC GAT ATC GTG GCC GGG GTT CCG TTG GGC AGC	555
Gln Gly Ala Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser	
95 100 105	
ATC AGC TTT GGC AGT CCG CTA CCT GCG GCA TAC GCA GAC AAC GTC GCA	603
Ile Ser Phe Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala	
110 115 120	
GCG GTC GCG GTC TTC GGC AAT CCG TCC AAC CGC GCC GGC GGA TCG CTG	651
Ala Val Ala Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu	
125 130 135 140	
TCG AGC CTG AGC CCG CTA TTC GGT TCC AAG GCG ATT GAC CTG TGC AAT	699
Ser Ser Leu Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn	
145 150 155	
CCC ACC GAT CCG ATC TGC CAT GTG GGC CCC GGC AAC GAA TTC AGC GGA	747
Pro Thr Asp Pro Ile Cys His Val Gly Pro Gly Asn Glu Phe Ser Gly	
160 165 170	
CAC ATC GAC GGC TAC ATA CCC ACC TAC ACC ACC CAG GCG GCT AGT TTC	795
His Ile Asp Gly Tyr Ile Pro Thr Tyr Thr Thr Glu Ala Ala Ser Phe	
175 180 185	
GTC GTG CAG AAG CTC GGC GCC GGG TCG GTG CCA CAT CTG CCT GGA TCC	843
Val Val Gln Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser	
190 195 200	
GTC CCG CAG CTG CCC GGG TCT GTC CTT CAG ATG CCC GGC ACT GCC GCA	891
Val Pro Gln Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala	
205 210 215 220	
CCG GCT CCC GAA TCG CTG CAC GGT CGC TGACGCTTTC TCAGTAAGCC CATAAAA	945
Pro Ala Pro Glu Ser Leu His Gly Arg	
225	
TCGCG	950

(2) INFORMATION FOR SEQ ID NO: 56;

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...33

164

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg Ala Gly Leu
      -10      -25      -20

Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile Ala Leu Gly
      -15      -10      -5

Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro Asp Ala Glu
      1          5          10          15

Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile Gly Arg Val
      20          25          30

Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly Met Glu Ile
      35          40          45

Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Gln Leu His Gly
      50          55          60

Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser Met Ala Ser
      65          70          75

Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser Gln Gly Ala
      80          85          90          95

Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser Ile Ser Phe
      100          105          110

Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala Ala Val Ala
      115          120          125

Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu Ser Ser Leu
      130          135          140

Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn Pro Thr Asp
      145          150          155

Pro Ile Cys His Val Gly Pro Gly Asn Glu Phe Ser Gly His Ile Asp
      160          165          170          175

Gly Tyr Ile Pro Thr Tyr Thr Thr Gln Ala Ala Ser Phe Val Val Gln
      180          185          190

Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser Val Pro Gln
      195          200          205

Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala Pro Ala Pro
      210          215          220

Glu Ser Leu His Gly Arg
      225

```

(2) INFORMATION FOR SEQ ID NO: 57:

105

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(4x) ~~FEATURE:~~

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 94...966
(C) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
(B) LOCATION: 94...264
(C) OTHER INFORMATION:

[41] SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CGAGGAGACC	GACGATCTCC	TCGACGAAAT	CGACGACGTC	CTCGAGGAMA	ACGCCGAGGA		60
CTTCGTCCGC	GCATACGTCC	AAAAGGGCGG	ACA GTG ACC TGG CCG TTG CCC GAT			114	
			Met Thr Trp Pro Leu Pro Asp				
			-55		-50		
CGC CTG TCC ATT AAT TCA CTC TCT GGA ACA CCC GCT GTA GAC CTA TCT						162	
Arg Leu Ser Ile Asn Ser Leu Ser Gly Thr Pro Ala Val Asp Leu Ser							
	-45		-40		-35		
TCT TTC ACT GAC TTC CTG CGC CGC CAG GCG CCG GAG TTG CTG CCG GCA						210	
Ser Phe Thr Asp Phe Leu Arg Arg Gln Ala Pro Gln Leu Leu Pro Ala							
	-30		-25		-20		
AGC ATC AGC GGC GGT GCG CCA CTC GCA GGC GGC GAT GCG CAA CTG CCG						258	
Ser Ile Ser Ser Gly Gly Ala Pro Leu Ala Gly Gly Asp Ala Gln Leu Pro							
	-15		-10		-5		
CAC GGC ACC ACC ATT GTC GCG CTG AAA TAC CCC GGC GGT GTT GTC ATG						306	
His Gly Thr Thr Ile Val Ala Leu Lys Tyr Pro Gly Gly Val Val Met							
1		5		10		15	
GCG GGT GAC CGG CGT TCG ACG CAG GCG AAC ATG ATT TCT GGG CGT GAT						354	
Ala Gly Asp Arg Arg Ser Thr Gln Gly Asn Met Ile Ser Gly Arg Asp							
	20		25		30		
GTG CGC AAG GTG TAT ATC ACC GGT GAC TAC ACC GCT ACC GGC ATC GCT						402	
Val Arg Lys Val Tyr Ile Thr Asp Asp Tyr Thr Ala Thr Gly Ile Ala							
	35		40		45		
GGC ACG GCT GCG GTC GCG GTT GAG TTT GCC CGG CTG TAT GCC GTG GAA						450	
Gly Thr Ala Ala Val Ala Val Glu Phe Ala Arg Leu Tyr Ala Val Glu							
	50		55		60		
CTT GAG CAC TAC GAG AAG CTC GAG GGT GTG CCG CTG ACC TTT GCC GGC						498	
Leu Glu His Tyr Glu Lys Leu Glu Gly Val Pro Leu Thr Phe Ala Gly							
65		70		75			

166

AAA ATC AAC CGG CTG GCG ATT ATG GTG CGT GGC AAT CTG GCG GCC GCG	546
Lys Ile Asn Arg Leu Ala Ile Met Val Arg Gly Asn Leu Ala Ala Ala	
80 85 90 95	
ATG CAG GGT CTG CTG GCG TTG CCG TTG CTG GCG GGC TAC GAC ATT CAT	594
Met Gln Gly Leu Leu Ala Leu Pro Leu Leu Ala Gly Tyr Asp Ile His	
100 105 110	
GCG TCT GAC CCG CAG AGC GCG GGT CGT ATC GTT TCG TTC GAC GCC GCC	642
Ala Ser Asp Pro Gln Ser Ala Gly Arg Ile Val Ser Phe Asp Ala Ala	
115 120 125	
GGC GGT TCG AAC ATC GAG GAA GAG GGC TAT CAG GCG GTG GGC TCG GGT	690
Gly Gly Trp Asn Ile Glu Glu Glu Gly Tyr Gln Ala Val Gly Ser Gly	
130 135 140	
TCG CTG TTC GCG AAG TCG TCG ATG AAG AAG TTG TAT TCG CAG GTT ACC	738
Ser Leu Phe Ala Lys Ser Ser Met Lys Lys Leu Tyr Ser Gln Val Thr	
145 150 155	
GAC GGT GAT TCG GGG CTG CCG GTG GCG GTC GAG GCG CTC TAC GAC GCC	786
Asp Gly Asp Ser Gly Leu Arg Val Ala Val Glu Ala Leu Tyr Asp Ala	
160 165 170 175	
GCC GAC GAC GAC TCC GCC ACC GGC GGT CCG GAC CTG GTG CCG GCC ATC	834
Ala Asp Asp Asp Ser Ala Thr Gly Gly Pro Asp Leu Val Arg Gly Ile	
180 185 190	
TTT CCG ACG GCG GTG ATC ATC GAC GCC GAC GCG GCG GTT GAC GTG CCG	882
Phe Pro Thr Ala Val Ile Ile Asp Ala Asp Gly Ala Val Asp Val Pro	
195 200 205	
GAG AGC CCG ATT GCC GAA TTG GCC CCG GCG ATC ATC GAA AGC CGT TCG	930
Glu Ser Arg Ile Ala Glu Leu Ala Arg Ala Ile Ile Glu Ser Arg Ser	
210 215 220	
GGT GCG GAT ACT TTC GGC TCC GAT GGC GGT GAG AAG TGAGTTTTCG GTATTT	982
Gly Ala Asp Thr Phe Gly Ser Asp Gly Gly Glu Lys	
225 230 235	
CATCTCGCCT GAGCAGGC	1000

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...56

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Met	Thr	Trp	Pro	Leu	Pro	Asp	Arg	Leu	Ser	Ile	Asn	Ser	Leu	Ser	Gly
-55						-50					-45				
Thr	Pro	Ala	Val	Asp	Leu	Ser	Ser	Phe	Thr	Asp	Phe	Leu	Arg	Arg	Gln
-40					-35					-30					-25
Ala	Pro	Glu	Leu	Leu	Pro	Ala	Ser	Ile	Ser	Gly	Gly	Ala	Pro	Leu	Ala
				-20					-15					-10	
Gly	Gly	Asp	Ala	Gln	Leu	Pro	His	Gly	Thr	Thr	Ile	Val	Ala	Leu	Lys
			-5					1				5			
Tyr	Pro	Gly	Gly	Val	Val	Met	Ala	Gly	Asp	Arg	Arg	Ser	Thr	Gln	Gly
	10					15					20				
Asn	Met	Ile	Ser	Gly	Arg	Asp	Val	Arg	Lys	Val	Tyr	Ile	Thr	Asp	Asp
25					30					35					40
Tyr	Thr	Ala	Thr	Gly	Ile	Ala	Gly	Thr	Ala	Ala	Val	Ala	Val	Glu	Phe
				45					50					55	
Ala	Arg	Leu	Tyr	Ala	Val	Glu	Leu	Glu	His	Tyr	Glu	Lys	Leu	Glu	Gly
			60					65					70		
Val	Pro	Leu	Thr	Phe	Ala	Gly	Lys	Ile	Asn	Arg	Leu	Ala	Ile	Met	Val
		75					80					85			
Arg	Gly	Asn	Leu	Ala	Ala	Ala	Met	Gln	Gly	Leu	Leu	Ala	Leu	Pro	Leu
	90					95					100				
Leu	Ala	Gly	Tyr	Asp	Ile	His	Ala	Ser	Asp	Pro	Gln	Ser	Ala	Gly	Arg
105					110					115					120
Ile	Val	Ser	Phe	Asp	Ala	Ala	Gly	Gly	Trp	Asn	Ile	Glu	Glu	Glu	Gly
				125					130					135	
Tyr	Gln	Ala	Val	Gly	Ser	Gly	Ser	Leu	Phe	Ala	Lys	Ser	Ser	Met	Lys
			140					145					150		
Lys	Leu	Tyr	Ser	Gln	Val	Thr	Asp	Gly	Asp	Ser	Gly	Leu	Arg	Val	Ala
	155						160					165			
Val	Glu	Ala	Leu	Tyr	Asp	Ala	Ala	Asp	Asp	Asp	Ser	Ala	Thr	Gly	Gly
	170					175					180				
Pro	Asp	Leu	Val	Arg	Gly	Ile	Phe	Pro	Thr	Ala	Val	Ile	Ile	Asp	Ala
185					190					195					200
Asp	Gly	Ala	Val	Asp	Val	Pro	Glu	Ser	Arg	Ile	Ala	Glu	Leu	Ala	Arg
				205					210					215	
Ala	Ile	Ile	Glu	Ser	Arg	Ser	Gly	Ala	Asp	Thr	Phe	Gly	Ser	Asp	Gly
			220					225					230		

158

Gly Glu Lys
235

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...808
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

TTGCCCCGCG CAGTCATCGA AAGCCGTTCC GGTGCGGATA CTTTCGGCTC CGATGGCGGT      60
GAGAA GTG AGT TTT CCG TAT TTC ATC TCG CCT GAG CAG GCG ATG CGC GAS      110
Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu
      1           5           10           15

CGC AGC GAG TTG GCG CTT AAG GGC ATT GCG CCG GCC AAA AGC GTG GTG      158
Arg Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val
      20           25           30

GCG CTG GCC TAT GCC GGT GGT GTG CTG TTC GTC GCG GAG AAT CCG TCG      206
Ala Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser
      35           40           45

CGG TCG CTG CAG AAG ATC AGT GAG CTC TAC GAT CCG GTG GGT TTT GCG      254
Arg Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala
      50           55           60

GCT GCG GGC AAG TTC AAC GAG TTC GAC AAT TTG CCG CCG GGC GGG ATC      302
Ala Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile
      65           70           75

CAG TTC GCC GAC ACC CGC GGT TAC GCC TAT GAC CGT CGT GAC GTC ACG      350
Gln Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr
      80           85           90           95

GGT CCG CAG TTG GCC AAT GTC TAC GCG CAG ACT CTA GGC ACC ATC TTC      398
Gly Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe
      100          105          110

ACC GAA CAG GCC AAG CCC TAC GAG GTT GAG TTG TGT GTG GCC GAG GTG      446
Thr Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val
      115          120          125

GCG CAT TAC GGC GAG ACG AAA CGC CCT GAG TTG TAT CCT ATT ACC TAC      494
Ala His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr
      130          135          140

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159

GAC GGG TCG ATC GCC GAC GAG CCG CAT TTC GTG GTG ATG GGC GGC ACC 542
 Asp Gly Ser Ile Ala Asp Glu Pro His Phe Val Val Met Gly Gly Thr
 145 150 155

ACG GAG CCG ATC GCC AAC GCG CTC AAA GAG TCG TAT GCC GAG AAC GGC 590
 Thr Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala
 160 165 170 175

AGC CTG ACC GAC GCC CTG CGT ATC GCG GTC GCT GCA TTS CCG GCC GGC 638
 Ser Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly
 180 185 190

AGT GCC GAC ACC TCG GGT GGT GAT CAA CCC ACC CTT GGC GTG GCC AGC 686
 Ser Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser
 195 200 205

TTA GAG GTG GCC GTT CTC GAT GCC AAC CCG CCA CCG CCG GCG TTC CCG 734
 Leu Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg
 210 215 220

CGC ATC ACC GGC TCC GCC CTG CAA GCG TTG CTG GTA GAC CAG GAA AGC 782
 Arg Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser
 225 230 235

CCG CAG TCT GAC GGC GAA TCG TCG GG CTGAGTCCGA AAGTCCGACG CGTGTCTG 836
 Pro Gln Ser Asp Gly Glu Ser Ser Gly
 240 245

GGACCCCGCT GCGACGTTAA CTGCGCCCTAA CCCCAGCTCG ACGCGTCGCC GCGCGTCTG 896

ACTT 900

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu Arg
 1 5 10 15

Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val Ala
 20 25 30

Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser Arg
 35 40 45

Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala Ala
 50 55 60

170

Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile Gln
 65 70 75 80
 Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr Gly
 85 90 95
 Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe Thr
 100 105 110
 Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val Ala
 115 120 125
 His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr Asp
 130 135 140
 Gly Ser Ile Ala Asp Glu Pro His Phe Val Val Met Gly Gly Thr Thr
 145 150 155 160
 Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala Ser
 165 170 175
 Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly Ser
 180 185 190
 Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser Leu
 195 200 205
 Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg Arg
 210 215 220
 Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser Pro
 225 230 235 240
 Gln Ser Asp Gly Glu Ser Ser Gly
 245

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1487
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTCATTGC CTGGTCGGGCG TCATTCCGTA CTATTCGGTT GTCGGACTTG ACCTACTGGG 60
 TCAGGCGGAC GAGCACTCGA CCATTAGGGT AGGGGCC GTG ACC CAC TAT GAC GTC 115
 Met Thr His Tyr Asp Val
 1 5

171

GTC	GTT	CTC	GGA	GCC	GGT	CCC	GGC	GGG	TAT	GTC	GCG	CCG	ATT	CGC	GCC	163
Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ala	Ala	Ile	Arg	Ala	
		10					15						20			
GCA	CAG	CTC	GGC	CTG	AGC	ACT	GCA	ATC	GTC	GAA	CCC	AAG	TAC	TGG	GGC	211
Ala	Gln	Leu	Gly	Leu	Ser	Thr	Ala	Ile	Val	Glu	Pro	Lys	Tyr	Trp	Gly	
	25					30					35					
GGA	GTA	TGC	CTC	AAT	GTC	GGC	TGT	ATC	CCA	TCC	AAG	GCG	CTG	TTG	CGC	259
Gly	Val	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	Arg	
	40				45					50						
AAC	GCC	GAA	CTG	GTC	CAC	ATC	TTC	ACC	AAG	GAC	GCC	AAA	GCA	TTT	GGC	307
Asn	Ala	Glu	Leu	Val	His	Ile	Phe	Thr	Lys	Asp	Ala	Lys	Ala	Phe	Gly	
55					60					65				70		
ATC	AGC	GGC	GAG	GTG	ACC	TTC	GAC	TAC	GGC	ATC	GCC	TAT	GAC	CGC	AGC	355
Ile	Ser	Gly	Glu	Val	Thr	Phe	Asp	Tyr	Gly	Ile	Ala	Tyr	Asp	Arg	Ser	
			75					80						85		
CGA	AAG	GTA	GCC	GAG	GGC	AGG	GTG	GCC	GGT	GTG	CAC	TTC	CTG	ATG	AAG	403
Arg	Lys	Val	Ala	Glu	Gly	Arg	Val	Ala	Gly	Val	His	Phe	Leu	Met	Lys	
		90					95						100			
AAG	AAC	AAG	ATC	ACC	GAG	ATC	CAC	GGG	TAC	GGC	ACA	TTT	GCC	GAC	GCC	451
Lys	Asn	Lys	Ile	Thr	Glu	Ile	His	Gly	Tyr	Gly	Thr	Phe	Ala	Asp	Ala	
	105					110						115				
AAC	ACG	TTG	TTG	GTT	GAT	CTC	AAC	GAC	GGC	GGT	ACA	GAA	TCG	GTC	ACG	499
Asn	Thr	Leu	Leu	Val	Asp	Leu	Asn	Asp	Gly	Gly	Thr	Glu	Ser	Val	Thr	
	120					125					130					
TTC	GAC	AAC	GCC	ATC	ATC	GCG	ACC	GGC	AGT	ACC	ACC	CGG	CTG	GTT	CCC	547
Phe	Asp	Asn	Ala	Ile	Ile	Ala	Thr	Gly	Ser	Ser	Thr	Arg	Leu	Val	Pro	
135					140					145					150	
GGC	ACC	TCA	CTG	TCG	GCC	AAC	GTA	GTC	ACC	TAC	GAG	GAA	CAG	ATC	CTG	595
Gly	Thr	Ser	Leu	Ser	Ala	Asn	Val	Val	Thr	Tyr	Glu	Glu	Gln	Ile	Leu	
			155						160					165		
TCC	CGA	GAG	CTG	CCG	AAA	TCG	ATC	ATT	ATT	GCC	GGA	GCT	GGT	GCC	ATT	643
Ser	Arg	Glu	Leu	Pro	Lys	Ser	Ile	Ile	Ile	Ala	Gly	Ala	Gly	Ala	Ile	
		170					175						180			
GGC	ATG	GAG	TTC	GGC	TAC	GTG	CTG	AAG	AAC	TAC	GCC	GTT	GAC	GTG	ACC	691
Gly	Met	Glu	Phe	Gly	Tyr	Val	Leu	Lys	Asn	Tyr	Gly	Val	Asp	Val	Thr	
	185					190						195				
ATC	GTG	GAA	TTC	CTT	CCG	CEG	GCG	CTG	CCC	AAC	GAG	GAC	GCC	GAT	GTG	739
Ile	Val	Glu	Phe	Leu	Pro	Arg	Ala	Leu	Pro	Asn	Glu	Asp	Ala	Asp	Val	
	200					205					210					
TCC	AAG	GAG	ATC	GAG	AAG	CAG	TTC	AAA	AAG	CTG	GGT	GTC	ACG	ATC	CTG	787
Ser	Lys	Glu	Ile	Glu	Lys	Gln	Phe	Lys	Lys	Leu	Gly	Val	Thr	Ile	Leu	
215					220					225					230	
ACC	GCC	ACG	AAG	GTC	GAG	TCC	ATC	GCC	GAT	GGC	GGG	TCG	CAG	GTC	ACC	835
Thr	Ala	Thr	Lys	Val	Glu	Ser	Ile	Ala	Asp	Gly	Gly	Ser	Gln	Val	Thr	

172

235					240					245									
GTG	ACC	GTC	ACC	AAG	GAC	GGC	GTG	GCG	CAA	GAG	CTT	AAG	GCG	GAA	AAG	883			
Val	Thr	Val	Thr	Lys	Asp	Gly	Val	Ala	Gln	Glu	Leu	Lys	Ala	Glu	Lys				
250					255					260									
GTG	TTG	CAG	GCC	ATC	GGA	TTT	GCG	CCC	AAC	GTC	GAA	GGG	TAC	GGG	CTG	931			
Val	Leu	Gln	Ala	Ile	Gly	Phe	Ala	Pro	Asn	Val	Glu	Gly	Tyr	Gly	Leu				
265					270					275									
GAC	AAG	GCA	GGC	GTC	GCG	CTG	ACC	GAC	GCG	AAG	GCT	ATC	GGT	GTC	GAC	979			
Asp	Lys	Ala	Gly	Val	Ala	Leu	Thr	Asp	Arg	Lys	Ala	Ile	Gly	Val	Asp				
280					285					290									
GAC	TAC	ATG	GGT	ACC	AAC	GTG	GGC	CAC	ATC	TAC	GCT	ATC	GGC	GAT	GTC	1027			
Asp	Tyr	Met	Arg	Thr	Asn	Val	Gly	His	Ile	Tyr	Ala	Ile	Gly	Asp	Val				
295					300					305					310				
AAT	GGA	TTA	CTG	CAG	CTG	GCG	CAC	GTC	GCC	GAG	GCA	CAA	GGC	GTG	GTA	1075			
Asn	Gly	Leu	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Val	Val				
315					320					325									
GCC	GCC	GAA	ACC	ATT	GCC	GGT	GCA	GAG	ACT	TTG	ACG	CTG	GGC	GAC	CAT	1123			
Ala	Ala	Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Leu	Thr	Leu	Gly	Asp	His				
330					335					340									
CGG	ATG	TTG	CCG	CGC	GCG	ACG	TTC	TGT	CAG	CCA	AAC	GTT	GCC	AGC	TTC	1171			
Arg	Met	Leu	Pro	Arg	Ala	Thr	Phe	Cys	Gln	Pro	Asn	Val	Ala	Ser	Phe				
345					350					355									
GGG	CTC	ACC	GAG	CAG	CAA	GCC	CGC	AAC	GAA	GGT	TAC	GAC	GTG	GTG	GTG	1219			
Gly	Leu	Thr	Glu	Gln	Gln	Ala	Arg	Asn	Glu	Gly	Tyr	Asp	Val	Val	Val				
360					365					370									
GCC	AAG	TTC	CCG	TTC	ACG	GCC	AAC	GCC	AAG	GCG	CAC	GSC	GTG	GGT	GAC	1267			
Ala	Lys	Phe	Pro	Phe	Thr	Ala	Asn	Ala	Lys	Ala	His	Gly	Val	Gly	Asp				
375					380					385					390				
CCC	AGT	GGG	TTC	GTC	AAG	CTG	GTG	GCC	GAC	GCC	AAG	CAC	GGC	GAG	CTA	1315			
Pro	Ser	Gly	Phe	Val	Lys	Leu	Val	Ala	Asp	Ala	Lys	His	Gly	Glu	Leu				
395					400					405									
CTG	GGT	GGG	CAC	CTG	GTC	GGC	CAC	GAC	GTG	GCC	GAG	CTG	CTG	CCG	GAG	1363			
Leu	Gly	Gly	His	Leu	Val	Gly	His	Asp	Val	Ala	Glu	Leu	Leu	Pro	Glu				
410					415					420									
CTC	ACG	CTG	GCG	CAG	AGG	TGG	GAC	CTG	ACC	GCC	AGC	GAG	CTG	GCT	CGC	1411			
Leu	Thr	Leu	Ala	Gln	Arg	Trp	Asp	Leu	Thr	Ala	Ser	Glu	Leu	Ala	Arg				
425					430					435									
AAC	GTC	CAC	ACC	CAC	CCA	ACG	ATG	TCT	GAG	GCG	CTG	CAG	GAG	TGC	TTC	1459			
Asn	Val	His	Thr	His	Pro	Thr	Met	Ser	Glu	Ala	Leu	Gln	Glu	Cys	Phe				
440					445					450									
CAC	GGC	CTG	GTT	GGC	CAC	ATG	ATC	AAT	T	TCTGAGCGGC	TCATGACGAG	GGCGG	1512						
His	Gly	Leu	Val	Gly	His	Met	Ile	Asn	Phe										
455					460														

CGAGCACTGA CACCCCCCAG ATCATCATGG GTGCCATCGG TGGTGTGG

1560

(3) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

Met Thr His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr
 1           5           10           15
Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Leu Ser Thr Ala Ile Val
 20           25           30
Glu Pro Lys Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro
 35           40           45
Ser Lys Ala Leu Leu Arg Asn Ala Glu Leu Val His Ile Phe Thr Lys
 50           55           60
Asp Ala Lys Ala Phe Gly Ile Ser Gly Glu Val Thr Phe Asp Tyr Gly
 65           70           75           80
Ile Ala Tyr Asp Arg Ser Arg Lys Val Ala Glu Gly Arg Val Ala Gly
 85           90           95
Val His Phe Leu Met Lys Lys Asn Lys Ile Thr Glu Ile His Gly Tyr
100          105          110
Gly Thr Phe Ala Asp Ala Asn Thr Leu Leu Val Asp Leu Asn Asp Gly
115          120          125
Gly Thr Glu Ser Val Thr Phe Asp Asn Ala Ile Ile Ala Thr Gly Ser
130          135          140
Ser Thr Arg Leu Val Pro Gly Thr Ser Leu Ser Ala Asn Val Val Thr
145          150          155          160
Tyr Glu Glu Gln Ile Leu Ser Arg Glu Leu Pro Lys Ser Ile Ile Ile
165          170          175
Ala Gly Ala Gly Ala Ile Gly Met Glu Phe Gly Tyr Val Leu Lys Asn
180          185          190
Tyr Gly Val Asp Val Thr Ile Val Glu Phe Leu Pro Arg Ala Leu Pro
195          200          205
Asn Glu Asp Ala Asp Val Ser Lys Glu Ile Glu Lys Gln Phe Lys Lys
210          215          220
Leu Gly Val Thr Ile Leu Thr Ala Thr Lys Val Glu Ser Ile Ala Asp
225          230          235          240
Gly Gly Ser Gln Val Thr Val Thr Val Thr Lys Asp Gly Val Ala Gln
245          250          255
Glu Leu Lys Ala Glu Lys Val Leu Gln Ala Ile Gly Phe Ala Pro Asn
260          265          270
Val Glu Gly Tyr Gly Leu Asp Lys Ala Gly Val Ala Leu Thr Asp Arg
275          280          285
Lys Ala Ile Gly Val Asp Asp Tyr Met Arg Thr Asn Val Gly His Ile
290          295          300
Tyr Ala Ile Gly Asp Val Asn Gly Leu Leu Gln Leu Ala His Val Ala
305          310          315          320
Glu Ala Gln Gly Val Val Ala Ala Glu Thr Ile Ala Gly Ala Glu Thr
325          330          335
Leu Thr Leu Gly Asp His Arg Met Leu Pro Arg Ala Thr Phe Cys Gln

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174

340	345	350
Pro Asn Val Ala Ser Phe Gly Leu Thr Glu Gln Gln Ala Arg Asn Glu		
355	360	365
Gly Tyr Asp Val Val Val Ala Lys Phe Pro Phe Thr Ala Asn Ala Lys		
370	375	380
Ala His Gly Val Gly Asp Pro Ser Gly Phe Val Lys Leu Val Ala Asp		
385	390	395
Ala Lys His Gly Glu Leu Leu Gly Gly His Leu Val Gly His Asp Val		
405	410	415
Ala Glu Leu Leu Pro Glu Leu Thr Leu Ala Gln Arg Tyr Asp Leu Thr		
420	425	430
Ala Ser Glu Leu Ala Arg Asn Val His Thr His Pro Thr Met Ser Glu		
435	440	445
Ala Leu Gln Glu Cys Phe His Gly Leu Val Gly His Met Ile Asn Phe		
450	455	460

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 101...490
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCCCCGCTC GCGCCCGCCC TGCAGGAARA GAGGCTCTGC CCAGGCCCCAG ACTCAGCCGA	60
GTAGTCACCC AGTACCCAC ACCAGGAAGG ACCGCCCATC ATG GCA AAG CTC TCC	115
	Met Ala Lys Leu Ser
	1 5
ACC GAC GAA CTG CTG GAC GCG TTC AAG GAA ATG ACC CTG TTG GAG CTC	163
Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met Thr Leu Leu Glu Leu	
	10 15 20
TCC GAC TTC GTC AAG AAG TTC GAG GAG ACC TTC GAG GTC ACC GCC GCC	211
Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe Glu Val Thr Ala Ala	
	25 30 35
GCT CCA GTC GCC GTC GCC GCC GCC GGT GCC GCC CCG GCC GGT GCC GCC	259
Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Pro Ala Gly Ala Ala	
	40 45 50
GTC GAG GCT GCC GAG GAG CAG TCC GAG TTC GAC GTG ATC CTT GAG GCC	307
Val Glu Ala Ala Glu Glu Gln Ser Glu Phe Asp Val Ile Leu Glu Ala	
	55 60 65
GCC GCC GAC AAG AAG ATC GGC GTC ATC AAG GTG GTC CCG GAG ATC GTT	355
Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val Val Arg Glu Ile Val	
	70 75 80 85

175

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TCC GGC CTG GGC CTC AAG GAG GCC AAG GAC CTG GTC GAC GGC GCG CCC      403
Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Asp Gly Ala Pro
          90                      95                      100

AAG CCG CTG CTG GAG AAG GTC GCC AAG GAG GCC GCC GAC GAG GCC AAG      451
Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala Ala Asp Glu Ala Lys
          105                      110                      115

GCC AAG CTG GAG GCC GCC GGC GCC ACC GTC ACC GTC AAG TAGCTCTGCC CA      503
Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr Val Lys
          120                      125                      130

GCGTGTTCCTT TTGGTCTGTC TCGGCCCGTA GCGAACACTG CGCCCGCT      550

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(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

Met Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
 1              5              10              15

Thr Leu Leu Glu Leu Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe
20              25              30

Glu Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala
35              40              45

Pro Ala Gly Ala Ala Val Glu Ala Ala Glu Glu Glu Ser Glu Phe Asp
50              55              60

Val Ile Leu Glu Ala Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val
65              70              75              80

Val Arg Glu Ile Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu
85              90              95

Val Asp Gly Ala Pro Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala
100             105             110

Ala Asp Glu Ala Lys Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr
115             120             125

Val Lys
130

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

176

(A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 87...770
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TGAACGCCCAT CGGGTCCAC GAACGCAGCG CTACCTGATC ACCACCGGGT CTGTTAGGGC	60
TCTTCCCCAG CTCCTACAGT CCGGCC ATG GCC ATT GAG GTT TCG GTG TTG CCG	113
Met Ala Ile Glu Val Ser Val Leu Arg	
1 5	
GTT TTC ACC GAT TCA GAC GGG AAT TTC GGT AAT CCG CTG GGG GTG ATC	161
Val Phe Thr Asp Ser Asp Gly Asn Phe Gly Asn Pro Leu Gly Val Ile	
10 15 20 25	
AAC GCC AGC AAG GTC GAA CAC CCG GAC AGG CAG CAG CTG GCA GCC CAA	209
Asn Ala Ser Lys Val Glu His Arg Asp Arg Gln Gln Leu Ala Ala Glu	
30 35 40	
TCG GGC TAC AGC GAA ACC ATA TTC GTC GAT CTT CCC AGC CCC GGC TCA	257
Ser Gly Tyr Ser Glu Thr Ile Phe Val Asp Leu Pro Ser Pro Gly Ser	
45 50 55	
ACC ACC GCA CAC GCC ACC ATC CAT ACT CCC CGC ACC GAA ATT CCG TTC	305
Thr Thr Ala His Ala Thr Ile His Thr Pro Arg Thr Glu Ile Pro Phe	
60 65 70	
GCC GGA CAC CCG ACC GTG GGA GCG TCC TGG TGG CTG CCC GAG AGG GGG	353
Ala Gly His Pro Thr Val Gly Ala Ser Trp Trp Leu Arg Glu Arg Gly	
75 80 85	
ACG CCA ATT AAC ACG CTG CAG GTG CCG GCC GGC ATC GTC CAG GTG AGC	401
Thr Pro Ile Asn Thr Leu Gln Val Pro Ala Gly Ile Val Gln Val Ser	
90 95 100 105	
TAC CAC GGT GAT CTC ACC GCC ATC AGC GCC CGC TCG GAA TGG GCA CCC	449
Tyr His Gly Asp Leu Thr Ala Ile Ser Ala Arg Ser Glu Trp Ala Pro	
110 115 120	
GAG TTC GCC ATC CAC GAC CTG GAT TCA CTT GAT GCG CTT GCC GCC GGC	497
Glu Phe Ala Ile His Asp Leu Asp Ser Leu Asp Ala Leu Ala Ala Ala	
125 130 135	
GAC CCC GCC GAC TTT CCG GAC GAC ATC GCG CAC TAC CTC TGG ACC TGG	545
Asp Pro Ala Asp Phe Pro Asp Asp Ile Ala His Tyr Leu Trp Thr Trp	
140 145 150	
ACC GAC CGC TCC GGT GGC TCG CTG CGC GCC CGC ATG TTT GGC GCC AAC	593
Thr Asp Arg Ser Ala Gly Ser Leu Arg Ala Arg Met Phe Ala Ala Asn	

177

155	160	165	
TTG GGC GTC ACC GAA GAC GAA GCG ACC GGT GCC GCG GCC ATC CGG ATT			641
Leu Gly Val Thr Glu Asp Glu Ala Thr Gly Ala Ala Ala Ile Arg Ile			
170	175	180	185
ACC GAT TAC CTC AGC CGT GAC CTC ACC ATC ACC CAG GGC AAA GGA TCG			689
Thr Asp Tyr Leu Ser Arg Asp Leu Thr Ile Thr Gln Gly Lys Gly Ser			
	190	195	200
TTG ATC CAC ACC ACC TGG AGT CCC GAG GGC TGG GTT CCG GTA GCC GGC			737
Leu Ile His Thr Thr Trp Ser Pro Glu Gly Trp Val Arg Val Ala Gly			
	205	210	215
CGA GTT GTC AGC GAC GGT GTG GCA CAA CTC GAC TGACCTAGAG CTCAGCGCTG			796
Arg Val Val Ser Asp Gly Val Ala Gln Leu Asp			
	220	225	
CCGATGCAAC ACGCGCGCAA GGTGATCCTG CAGGGGTGGC CCGACCGCGC GCATCTGCAA			856
CGAGTACGAA AGCTCGTCGC COTCGATGCG GTAGGAACGG TCAAGCGCGG			906

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met	Ala	Ile	Glu	Val	Ser	Val	Leu	Arg	Val	Phe	Thr	Asp	Ser	Asp	Gly
1				5					10					15	
Asn	Phe	Gly	Asn	Pro	Leu	Gly	Val	Ile	Asn	Ala	Ser	Lys	Val	Gln	His
		20					25						30		
Arg	Asp	Arg	Gln	Gln	Leu	Ala	Ala	Gln	Ser	Gly	Tyr	Ser	Glu	Thr	Ile
		35				40						45			
Phe	Val	Asp	Leu	Pro	Ser	Pro	Gly	Ser	Thr	Thr	Ala	His	Ala	Thr	Ile
	50					55				60					
His	Thr	Pro	Arg	Thr	Glu	Ile	Pro	Phe	Ala	Gly	His	Pro	Thr	Val	Gly
65				70					75					80	
Ala	Ser	Trp	Trp	Leu	Arg	Glu	Arg	Gly	Thr	Pro	Ile	Asn	Thr	Leu	Gln
			85				90						95		
Val	Pro	Ala	Gly	Ile	Val	Gln	Val	Ser	Tyr	His	Gly	Asp	Leu	Thr	Ala
	100						105					110			
Ile	Ser	Ala	Arg	Ser	Glu	Trp	Ala	Pro	Glu	Phe	Ala	Ile	His	Asp	Leu

178

115	120	125
Asp Ser Leu Asp Ala Leu Ala Ala Asp Pro Ala Asp Phe Pro Asp		
130	135	140
Asp Ile Ala His Tyr Leu Trp Thr Trp Thr Asp Arg Ser Ala Gly Ser		
145	150	155
Leu Arg Ala Arg Met Phe Ala Ala Asn Leu Gly Val Thr Glu Asp Glu		
	165	170
Ala Thr Gly Ala Ala Ala Ile Arg Ile Thr Asp Tyr Leu Ser Arg Asp		
	180	185
Leu Thr Ile Thr Gln Gly Lys Gly Ser Leu Ile His Thr Thr Trp Ser		
	195	200
Pro Glu Gly Trp Val Arg Val Ala Gly Arg Val Val Ser Asp Gly Val		
	210	215
Ala Gln Leu Asp		
225		

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...485
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTTGTGGTG TCGTGGGTCT GGGGGGGCGCC AACTGGGATT CGGTGGG GTG GGT GCA	57
Met Gly Ala	
1	
GGT CCG GCG ATG GGC ATC GGA GGT GTG GGT GGT TTG GGT GCG GCC GGT	105
Gly Pro Ala Met Gly Ile Gly Gly Val Gly Gly Leu Gly Gly Ala Gly	
5 10 15	
TCG GGT CCG GCG ATG GGC ATG GGG GGT GTG GGT GGT TTG GGT GCG GCC	153
Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu Gly Gly Ala	
20 25 30 35	
GGT TCG GGT CCG GCG ATG GGC ATG GGG GGT GTG GGT GGT TTA GAT GCG	201
Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu Asp Ala	
40 45 50	
GCC GGT TCC GGC GAG GGC GGC TCT CCT GCG GCG ATC GGC ATC GGA GTT	249

179

Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly Ile Gly Val	
55 60 65	
GGC GGA GGC GGA GGT GGG GGT GGG GGT GGC GGC GGC GGC GGC GAC ACG	297
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Asp Thr	
70 75 80	
AAC CGC TCC GAC AGG TCG TCG GAC GTC GGG GGC GGA GTC TGG CCG TTG	345
Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Gly Val Trp Pro Leu	
85 90 95	
GGC TTC GGT AGG TTT GCC GAT GCG GGC GCC GGC GGA AAC GAA GCA CTG	393
Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn Glu Ala Leu	
100 105 110 115	
GGG TCG AAG AAC GGC TGC GCT GCC ATA TCG TCC GGA GCT TCC ATA CCT	441
Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala Ser Ile Pro	
120 125 130	
TCG TGC GGC CGG AAG ACC TTG TCG TAGTCGGCCG CCATGACAAC CTCTCAGAGT	495
Ser Cys Gly Arg Lys Ser Leu Ser	
135	
GCGCT	500

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Met Gly Ala Gly Pro Ala Met Gly Ile Gly Gly Val Gly Gly Leu Gly	
1 5 10 15	
Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu	
20 25 30	
Gly Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly	
35 40 45	
Leu Asp Ala Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly	
50 55 60	
Ile Gly Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
65 70 75 80	
Ala Asp Thr Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Gly Val	
85 90 95	
Trp Pro Leu Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn	

180

100	105	110
Glu Ala Leu Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala		
115	120	125
Ser Ile Pro Ser Cys Gly Arg Lys Ser Leu Ser		
130	135	

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...2019
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGCGCACTCT GAGAGGTTGT C ATG GCG GCC GAC TAC GAC AAG CTC TTC CCG	51
Met Ala Ala Asp Tyr Asp Lys Leu Phe Arg	
1 5 10	
CCG CAC GAA SST ATG GAA GCT CCG GAC GAT ATG GCA GCG CAG CCG TTC	99
Pro His Glu Gly Met Glu Ala Pro Asp Asp Met Ala Ala Gln Pro Phe	
15 20 25	
TTC GAC CCC AGT GCT TCG TTT CCG CCG GCG CCC GCA TCG GCA AAC CTA	147
Phe Asp Pro Ser Ala Ser Phe Pro Pro Ala Pro Ala Ser Ala Asn Leu	
30 35 40	
CCG AAG CCC AAC GGC CAG ACT CCG CCC CCG ACG TCC GAC GAC CTG TCG	195
Pro Lys Pro Asn Gly Gln Thr Pro Pro Pro Thr Ser Asp Asp Leu Ser	
45 50 55	
GAG CCG TTC GTG TCG GCC CCG CCG CCG CCA CCC CCA CCC CCA CCT CCG	243
Glu Arg Phe Val Ser Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro	
60 65 70	
CCT CCG CCA ACT CCG ATG CCG ATC GCC GCA GGA GAG CCG CTC TCG CCG	291
Pro Pro Pro Thr Pro Met Pro Ile Ala Ala Gly Glu Pro Pro Ser Pro	
75 80 85 90	
GAA CCG GCC GCA TCT AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC GGA	339
Glu Pro Ala Ala Ser Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly	
95 100 105	
CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC	387
Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile Ala	
110 115 120	

181

GGA CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCT CCG ATG CCC ATC	438
Gly Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile	
125 130 135	
GCC GGA CCT GCA CCC ACC CCA ACC GAA TCC CAG TTG GCG CCC CCC AGA	483
Ala Gly Pro Ala Pro Thr Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg	
140 145 150	
CCA CCG ACA CCA CAA ACG CCA ACC GGA GCG CCG CAG CAA CCG GAA TCA	531
Pro Pro Thr Pro Gln Thr Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser	
155 160 165 170	
CCG GCG CCC CAC GTA CCC TCG CAC GCG CCA CAT CAA CCC CCG CGC ACC	579
Pro Ala Pro His Val Pro Ser His Gly Pro His Gln Pro Arg Arg Thr	
175 180 185	
GCA CCA GCA CCG CCC TGG GCA AAG ATG CCA ATC GGC GAA CCC CCG CCC	627
Ala Pro Ala Pro Pro Trp Ala Lys Met Pro Ile Gly Glu Pro Pro Pro	
190 195 200	
GCT CCG TCC AGA CCG TCT GCG TCC CCG GCC GAA CCA CCG ACC CCG CCT	675
Ala Pro Ser Arg Pro Ser Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro	
205 210 215	
GCC CCC CAA CAC TCC CGA CGT GCG CGC CCG GGT CAC CGC TAT CGC ACA	723
Ala Pro Gln His Ser Arg Arg Ala Arg Arg Gly His Arg Tyr Arg Thr	
220 225 230	
GAC ACC GAA CGA AAC GTC GGG AAG GTA GCA ACT GGT CCA TCC ATC CAG	771
Asp Thr Glu Arg Asn Val Gly Lys Val Ala Thr Gly Pro Ser Ile Gln	
235 240 245 250	
GCG CCG CTG CCG GCA GAG GAA GCA TCC GGC GCG CAG CTC GCC CCC GGA	819
Ala Arg Leu Arg Ala Glu Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly	
255 260 265	
ACG GAG CCC TCG CCA GCG CCG TTG GGC CAA CCG AGA TCG TAT CTG GCT	867
Thr Glu Pro Ser Pro Ala Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala	
270 275 280	
CCG CCC ACC CGC CCC GCG CCG ACA GAA CCT CCC CCC ACC CCC TCG CCG	915
Pro Pro Thr Arg Pro Ala Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro	
285 290 295	
CAG CGC AAC TCC GGT CCG CGT GCC GAG CGA CGC GTC CAC CCC GAT TTA	963
Gln Arg Asn Ser Gly Arg Arg Ala Glu Arg Arg Val His Pro Asp Leu	
300 305 310	
GCC GCC CAA CAT GCC GCG GCG CAA CCT GAT TCA ATT ACG GCC GCA ACC	1011
Ala Ala Gln His Ala Ala Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr	
315 320 325 330	
ACT GGC GGT CGT CGC CGC AAG CGT GCA GCG CCG GAT CTC GAC GCG ACA	1059
Thr Gly Gly Arg Arg Arg Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr	
335 340 345	
CAG AAA TCC TTA AGG CCG GCG GCC AAG GGG CCG AAG GTG AAG AAG GTG	1107
Gln Lys Ser Leu Arg Pro Ala Ala Lys Gly Pro Lys Val Lys Lys Val	

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350			355			360											
AAG	CCC	CAG	AAA	CCG	AAG	GCC	ACG	AAG	CCG	CCC	AAA	GTG	GTG	TCG	CAG		1155
Lys	Pro	Gln	Lys	Pro	Lys	Ala	Thr	Lys	Pro	Pro	Lys	Val	Val	Ser	Gln		
		365					370						375				
CGC	GGC	TGG	CGA	CAT	TGG	GTG	CAT	GCG	TTG	ACG	CGA	ATC	AAC	CTG	GGC		1203
Arg	Gly	Trp	Arg	His	Trp	Val	His	Ala	Leu	Thr	Arg	Ile	Asn	Leu	Gly		
		380				385						390					
CTG	TCA	CCC	GAC	GAG	AAG	TAC	GAG	CTG	GAC	CTG	CAC	GCT	CGA	GTC	CGC		1251
Leu	Ser	Pro	Asp	Glu	Lys	Tyr	Glu	Leu	Asp	Leu	His	Ala	Arg	Val	Arg		
		395			400					405					410		
CGC	AAT	CCC	CGC	GGG	TCG	TAT	CAG	ATC	GCC	GTC	GTC	GGT	CTC	AAA	GGT		1299
Arg	Asn	Pro	Arg	Gly	Ser	Tyr	Gln	Ile	Ala	Val	Val	Gly	Leu	Lys	Gly		
				415					420					425			
GGG	GCT	GGC	AAA	ACC	ACG	CTG	ACA	GCA	GCG	TTG	GGG	TCG	ACG	TTG	GCT		1347
Gly	Ala	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Leu	Gly	Ser	Thr	Leu	Ala		
			430					435					440				
CAG	GTG	CGG	GCC	GAC	CGG	ATC	CTG	GCT	CTA	GAC	GCG	GAT	CCA	GGC	GCC		1395
Gln	Val	Arg	Ala	Asp	Arg	Ile	Leu	Ala	Leu	Asp	Ala	Asp	Pro	Gly	Ala		
		445					450					455					
GGA	AAC	CTC	GCC	GAT	CGG	GTA	GGG	CGA	CAA	TCG	GGC	GCG	ACC	ATC	GCT		1443
Gly	Asn	Leu	Ala	Asp	Arg	Val	Gly	Arg	Gln	Ser	Gly	Ala	Thr	Ile	Ala		
		460				465					470						
GAT	GTG	CTT	GCA	GAA	AAA	GAG	CTG	TCG	CAC	TAC	AAC	GAC	ATC	CGC	GCA		1491
Asp	Val	Leu	Ala	Glu	Lys	Glu	Leu	Ser	His	Tyr	Asn	Asp	Ile	Arg	Ala		
		475			480					485					490		
CAC	ACT	AGC	GTC	AAT	GCG	GTC	AAT	CTG	GAA	GTG	CTG	CCG	GCA	CCG	GAA		1539
His	Thr	Ser	Val	Asn	Ala	Val	Asn	Leu	Glu	Val	Leu	Pro	Ala	Pro	Glu		
				495				500					505				
TAC	AGC	TCG	GCG	CAG	CGC	GCG	CTC	AGC	GAC	GCC	GAC	TGG	CAT	TTC	ATC		1587
Tyr	Ser	Ser	Ala	Gln	Arg	Ala	Leu	Ser	Asp	Ala	Asp	Trp	His	Phe	Ile		
			510				515						520				
GCC	GAT	CCT	GCG	TCG	AGG	TTT	TAC	AAC	CTC	GTC	TTG	GCT	GAT	TGT	GGG		1635
Ala	Asp	Pro	Ala	Ser	Arg	Phe	Tyr	Asn	Leu	Val	Leu	Ala	Asp	Cys	Gly		
		525					530					535					
GCC	GGC	TTC	TTC	GAC	CCG	CTG	ACC	CGC	GCG	GTG	CTG	TCC	ACG	GTG	TCC		1683
Ala	Gly	Phe	Phe	Asp	Pro	Leu	Thr	Arg	Gly	Val	Leu	Ser	Thr	Val	Ser		
		540				545					550						
GGT	GTC	GTG	GTC	GTG	GCA	AGT	GTC	TCA	ATC	GAC	GGC	GCA	CAA	CAG	GCG		1731
Gly	Val	Val	Val	Val	Ala	Ser	Val	Ser	Ile	Asp	Gly	Ala	Gln	Gln	Ala		
		555			560					565					570		
TCG	GTC	GCG	TTG	GAC	TGG	TTG	CGC	AAC	AAC	GGT	TAC	CAA	GAT	TTG	GCG		1775
Ser	Val	Ala	Leu	Asp	Trp	Leu	Arg	Asn	Asn	Gly	Tyr	Gln	Asp	Leu	Ala		
			575				580						585				

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AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT      1827
Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn
      590                      595                      600

GTC GCA GTT AAA GAC CTG GTS CGG CAT TTC GAA CAG CAA GTT CAA CCC      1875
Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro
      605                      610                      615

GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC      1923
Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr
      620                      625                      630

GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC      1971
Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu
      635                      640                      645                      650

GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T      2020
Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg
      655                      660                      665

GAGCGCACCT GCTGTGCTG CTGGTCTAC      2050

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(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

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Met Ala Ala Asp Tyr Asp Lys Leu Phe Arg Pro His Glu Gly Met Glu
 1                      5                      10                      15

Ala Pro Asp Asp Met Ala Ala Gln Pro Phe Phe Asp Pro Ser Ala Ser
20                      25                      30

Phe Pro Pro Ala Pro Ala Ser Ala Asn Leu Pro Lys Pro Asn Gly Gln
35                      40                      45

Thr Pro Pro Pro Thr Ser Asp Asp Leu Ser Glu Arg Phe Val Ser Ala
50                      55                      60

Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Thr Pro Met
65                      70                      75                      80

Pro Ile Ala Ala Gly Glu Pro Pro Ser Pro Glu Pro Ala Ala Ser Lys
85                      90                      95

Pro Pro Thr Pro Pro Met Pro Ile Ala Gly Pro Glu Pro Ala Pro Pro
100                      105                      110

Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly Pro Glu Pro Ala Pro

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115	120	125
Pro Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly Pro Ala Pro Thr 130	135	140
Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg Pro Pro Thr Pro Gln Thr 145	150	155
Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser Pro Ala Pro His Val Pro 165	170	175
Ser His Gly Pro His Gln Pro Arg Arg Thr Ala Pro Ala Pro Pro Trp 180	185	190
Ala Lys Met Pro Ile Gly Glu Pro Pro Pro Ala Pro Ser Arg Pro Ser 195	200	205
Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro Ala Pro Gln His Ser Arg 210	215	220
Arg Ala Arg Arg Gly His Arg Tyr Arg Thr Asp Thr Glu Arg Asn Val 225	230	235
Gly Lys Val Ala Thr Gly Pro Ser Ile Gln Ala Arg Leu Arg Ala Glu 245	250	255
Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly Thr Glu Pro Ser Pro Ala 260	265	270
Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala Pro Pro Thr Arg Pro Ala 275	280	285
Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro Gln Arg Asn Ser Gly Arg 290	295	300
Arg Ala Glu Arg Arg Val His Pro Asp Leu Ala Ala Gln His Ala Ala 305	310	315
Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr Thr Gly Gly Arg Arg Arg 325	330	335
Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr Gln Lys Ser Leu Arg Pro 340	345	350
Ala Ala Lys Gly Pro Lys Val Lys Lys Val Lys Pro Gln Lys Pro Lys 355	360	365
Ala Thr Lys Pro Pro Lys Val Val Ser Gln Arg Gly Trp Arg His Trp 370	375	380
Val His Ala Leu Thr Arg Ile Asn Leu Gly Leu Ser Pro Asp Glu Lys 385	390	395
Tyr Glu Leu Asp Leu His Ala Arg Val Arg Arg Asn Pro Arg Gly Ser 405	410	415
Tyr Gln Ile Ala Val Val Gly Leu Lys Gly Gly Ala Gly Lys Thr Thr 420	425	430

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Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala Gln Val Arg Ala Asp Arg
  435                      440                      445

Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala Gly Asn Leu Ala Asp Arg
  450                      455                      460

Val Gly Arg Gln Ser Gly Ala Thr Ile Ala Asp Val Leu Ala Glu Lys
  465                      470                      475                      480

Glu Leu Ser His Tyr Asn Asp Ile Arg Ala His Thr Ser Val Asn Ala
      485                      490                      495

Val Asn Leu Glu Val Leu Pro Ala Pro Glu Tyr Ser Ser Ala Gln Arg
      500                      505                      510

Ala Leu Ser Asp Ala Asp Trp His Phe Ile Ala Asp Pro Ala Ser Arg
  515                      520                      525

Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly Ala Gly Phe Phe Asp Pro
  530                      535                      540

Leu Thr Arg Gly Val Leu Ser Thr Val Ser Gly Val Val Val Val Ala
  545                      550                      555                      560

Ser Val Ser Ile Asp Gly Ala Gln Gln Ala Ser Val Ala Leu Asp Trp
      565                      570                      575

Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala Ser Arg Ala Cys Val Val
      580                      585                      590

Ile Asn His Ile Met Pro Gly Glu Pro Asn Val Ala Val Lys Asp Leu
  595                      600                      605

Val Arg His Phe Glu Gln Gln Val Gln Pro Gly Arg Val Val Val Met
  610                      615                      620

Pro Trp Asp Arg His Ile Ala Ala Gly Thr Glu Ile Ser Leu Asp Leu
  625                      630                      635                      640

Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu Glu Leu Ala Ala Ala Leu
      645                      650                      655

Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg
      660                      665

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(3) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1851

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GCACCGATGA GGAGGAGCGG CGCCAACGGC CCGCGCGCGC GACGATGCAA AGCGCAGCGA	60
TGAGGAGGAG CCGCGCGC ATG ACT GCT GAA CCG GAA GTA CCG ACG CTG CGC Met Thr Ala Glu Pro Glu Val Arg Thr Leu Arg 1 5 10	111
GAG GTT GTG CTG GAC CAG CTC GGC ACT GCT GAA TCG CGT GCG TAC AAG Glu Val Val Leu Asp Gln Leu Gly Thr Ala Glu Ser Arg Ala Tyr Lys 15 20 25	159
ATG TGG CTG CCG CCG TTG ACC AAT CCG GTC CCG CTC AAC GAG CTC ATC Met Trp Leu Pro Pro Leu Thr Asn Pro Val Pro Leu Asn Glu Leu Ile 30 35 40	207
GCC CGT GAT CCG CGA CAA CCC CTG CGA TTT GCC CTG GGG ATC ATG GAT Ala Arg Asp Arg Arg Gln Pro Leu Arg Phe Ala Leu Gly Ile Met Asp 45 50 55	255
GAA CCG CGC CGC CAT CTA CAG GAT GTG TGG GGC GTA GAC GTT TCC GGG Glu Pro Arg Arg His Leu Gln Asp Val Trp Gly Val Asp Val Ser Gly 60 65 70 75	303
GCC GGC GGC AAC ATC GGT ATT GGG GGC GCA CCT CAA ACC GGG AAG TCG Ala Gly Gly Asn Ile Gly Ile Gly Gly Ala Pro Gln Thr Gly Lys Ser 80 85 90	351
ACG CTA CTG CAG ACG ATG GTG ATG TCG GCC GCC GCC ACA CAC TCA CCG Thr Leu Leu Gln Thr Met Val Met Ser Ala Ala Ala Thr His Ser Pro 95 100 105	399
CGC AAC GTT CAG TTC TAT TGC ATC GAC CTA GGT GGC GGC GGG CTG ATC Arg Asn Val Gln Phe Tyr Cys Ile Asp Leu Gly Gly Gly Gly Leu Ile 110 115 120	447
TAT CTC GAA AAC CTT CCA CAC GTC GGT GGG GTA GCC AAT CCG TCC GAG Tyr Leu Glu Asn Leu Pro His Val Gly Gly Val Ala Asn Arg Ser Glu 125 130 135	495
CCC GAC AAG GTC AAC CCG GTG GTC GCA GAG ATG CAA GCC GTC ATG CCG Pro Asp Lys Val Asn Arg Val Val Ala Glu Met Gln Ala Val Met Arg 140 145 150 155	543
CAA CCG GAA ACC ACC TTC AAG GAA CAC CGA GTG GGC TCG ATC GGG ATG Gln Arg Glu Thr Thr Phe Lys Glu His Arg Val Gly Ser Ile Gly Met 160 165 170	591
TAC CCG CAG CTG CGT GAC GAT CCA AGT CAA CCC GTT GCG TCC GAT CCA Tyr Arg Gln Leu Arg Asp Asp Pro Ser Gln Pro Val Ala Ser Asp Pro 175 180 185	639
TAC GGC GAC GTC TTT CTG ATC ATC GAC GGA TGG CCC GGT TTT GTC GGC Tyr Gly Asp Val Phe Leu Ile Ile Asp Gly Trp Pro Gly Phe Val Gly 190 195 200	687

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GAG TTC CCC GAC CTT GAG GGG CAG GTT CAA GAT CTG GCC GCC CAG GGG	735
Glu Phe Pro Asp Leu Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly	
205 210 215	
CTG GGG TTC GGC GTC CAC GTC ATC ATC TCC ACC CCA CGC TGG ACA GAG	783
Leu Gly Phe Gly Val His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu	
220 225 230 235	
CTG AAG TCG CGT GTT CGC GAC TAC CTC GGC ACC AAG ATC GAG TTC CGG	831
Leu Lys Ser Arg Val Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg	
240 245 250	
CTT GGT GAC GTC AAT GAA ACC CAG ATC GAC CGG ATT ACC CGC GAG ATC	879
Leu Gly Asp Val Asn Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile	
255 260 265	
CCG GCG AAT CGT CCG GGT CGG GCA GTG TCG ATG GAA AAG CAC CAT CTG	927
Pro Ala Asn Arg Pro Gly Arg Ala Val Ser Met Glu Lys His His Leu	
270 275 280	
ATG ATC GGC GTG CCC AGG TTC GAC GGC GTG CAC AGC GCC GAT AAC CTG	975
Met Ile Gly Val Pro Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu	
285 290 295	
GTG GAG GCG ATC ACC GCG GGG GTG ACG CAG ATC GCT TCC CAG CAC ACC	1023
Val Glu Ala Ile Thr Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr	
300 305 310 315	
GAA CAG GCA CCT CCG GTG CCG GTC CTG CCG GAG CGT ATC CAC CTG CAC	1071
Glu Gln Ala Pro Pro Val Arg Val Leu Pro Glu Arg Ile His Leu His	
320 325 330	
GAA CTC GAC CCG AAC CCG CCG GGA CCA GAG TCC GAC TAC CGC ACT CGC	1119
Glu Leu Asp Pro Asn Pro Pro Gly Pro Glu Ser Asp Tyr Arg Thr Arg	
335 340 345	
TGG GAG ATT CCG ATC GGC TTG CGC GAG ACG GAC CTG ACG CCG GCT CAC	1167
Trp Glu Ile Pro Ile Gly Leu Arg Glu Thr Asp Leu Thr Pro Ala His	
350 355 360	
TGC CAC ATG CAC ACG AAC CCG CAC CTA CTG ATC TTC GGT GCG GCC AAA	1215
Cys His Met His Thr Asn Pro His Leu Leu Ile Phe Gly Ala Ala Lys	
365 370 375	
TGG GGC AAG ACG ACC ATT GCC CAC GCG ATC GCG CGC GCC ATT TGT GCC	1263
Ser Gly Lys Thr Thr Ile Ala His Ala Ile Ala Arg Ala Ile Cys Ala	
380 385 390 395	
CGA AAC AGT CCC CAG CAG GTG CCG TTC ATG CTC GCG GAC TAC CGC TCG	1311
Arg Asn Ser Pro Gln Gln Val Arg Phe Met Leu Ala Asp Tyr Arg Ser	
400 405 410	
GGC CTG CTG GAC GCG GTG CCG GAC ACC CAT CTG CTG GGC GCC GCG GCG	1359
Gly Leu Leu Asp Ala Val Pro Asp Thr His Leu Leu Gly Ala Gly Ala	
415 420 425	
ATC AAC CGC AAC AGC GCG TCG CTA GAC GAG GCC GCT CAA GCA CTG GCG	1407
Ile Asn Arg Asn Ser Ala Ser Leu Asp Glu Ala Ala Gln Ala Leu Ala	

188

430	435	440	
GTC AAC CTG AAG AAG CGG TTG CCG CCG ACC GAC CTG ACG ACG GCG CAG			1495
Val Asn Leu Lys Lys Arg Leu Pro Pro Thr Asp Leu Thr Thr Ala Gln			
445	450	455	
CTA CGC TCG CGT TCG TGG TGG AGC GGA TTT GAC GTC GTG CTT CTG GTC			1503
Leu Arg Ser Arg Ser Trp Trp Ser Gly Phe Asp Val Val Leu Leu Val			
460	465	470	475
GAC GAT TGG CAC ATG ATC GTG GGT GCC GCC GGG GGG ATG CCG CCG ATG			1551
Asp Asp Trp His Met Ile Val Gly Ala Ala Gly Gly Met Pro Pro Met			
	480	485	490
GCA CCG CTG GCC CCG TTA TTG CCG GCG GCG GCA GAT ATC GGG TTG CAC			1599
Ala Pro Leu Ala Pro Leu Leu Pro Ala Ala Ala Asp Ile Gly Leu His			
	495	500	505
ATC ATT GTC ACC TGT CAG ATG ASC CAG GCT TAC AAG GCA ACC ATG GAC			1647
Ile Ile Val Thr Cys Gln Met Ser Gln Ala Tyr Lys Ala Thr Met Asp			
	510	515	520
AAG TTC GTC GGC GCC GCA TTC GGG TCG GGC GCT CCG ACA ATG TTC CTT			1695
Lys Phe Val Gly Ala Ala Phe Gly Ser Gly Ala Pro Thr Met Phe Leu			
	525	530	535
TCG GGC GAG AAG CAG GAA TTC CCA TCC AGT GAG TTC AAG GTC AAG CGG			1743
Ser Gly Glu Lys Gln Glu Phe Pro Ser Ser Glu Phe Lys Val Lys Arg			
540	545	550	555
CGC CCC CCT GGC CAG GCA TTT CTC GTC TCG CCA GAC GGC AAA GAG GTC			1791
Arg Pro Pro Gly Gln Ala Phe Leu Val Ser Pro Asp Gly Lys Glu Val			
	560	565	570
ATC CAG GCC CCC TAC ATC GAG CCT CCA GAA GAA GTG TTC GCA GCA CCC			1839
Ile Gln Ala Pro Tyr Ile Glu Pro Pro Glu Glu Val Phe Ala Ala Pro			
	575	580	585
CCA AGC GCC GGT TAGATTATT TCATTCCCGG TGTAGCAGGA CCGAGCTC			1890
Pro Ser Ala Gly			
	590		

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Met	Thr	Ala	Glu	Pro	Glu	Val	Arg	Thr	Leu	Arg	Glu	Val	Val	Leu	Asp
1				5					10					15	

189

Gln Leu Gly Thr Ala Glu Ser Arg Ala Tyr Lys Met Trp Leu Pro Pro
 20 25 30
 Leu Thr Asn Pro Val Pro Leu Asn Glu Leu Ile Ala Arg Asp Arg Arg
 35 40 45
 Gln Pro Leu Arg Phe Ala Leu Gly Ile Met Asp Glu Pro Arg Arg His
 50 55 60
 Leu Gln Asp Val Trp Gly Val Asp Val Ser Gly Ala Gly Gly Asn Ile
 65 70 75 80
 Gly Ile Gly Gly Ala Pro Gln Thr Gly Lys Ser Thr Leu Leu Gln Thr
 85 90 95
 Met Val Met Ser Ala Ala Ala Thr His Ser Pro Arg Asn Val Gln Phe
 100 105 110
 Tyr Cys Ile Asp Leu Gly Gly Gly Gly Leu Ile Tyr Leu Glu Asn Leu
 115 120 125
 Pro His Val Gly Gly Val Ala Asn Arg Ser Glu Pro Asp Lys Val Asn
 130 135 140
 Arg Val Val Ala Glu Met Gln Ala Val Met Arg Gln Arg Glu Thr Thr
 145 150 155 160
 Phe Lys Glu His Arg Val Gly Ser Ile Gly Met Tyr Arg Gln Leu Arg
 165 170 175
 Asp Asp Pro Ser Gln Pro Val Ala Ser Asp Pro Tyr Gly Asp Val Phe
 180 185 190
 Leu Ile Ile Asp Gly Trp Pro Gly Phe Val Gly Glu Phe Pro Asp Leu
 195 200 205
 Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly Leu Gly Phe Gly Val
 210 215 220
 His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu Leu Lys Ser Arg Val
 225 230 235 240
 Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg Leu Gly Asp Val Asn
 245 250 255
 Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile Pro Ala Asn Arg Pro
 260 265 270
 Gly Arg Ala Val Ser Met Glu Lys His His Leu Met Ile Gly Val Pro
 275 280 285
 Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu Val Glu Ala Ile Thr
 290 295 300
 Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr Glu Gln Ala Pro Pro
 305 310 315 320
 Val Arg Val Leu Pro Glu Arg Ile His Leu His Glu Leu Asp Pro Asn

190

	325		330		335										
Pro	Pro	Gly	Pro	Glu	Ser	Asp	Tyr	Arg	Thr	Arg	Trp	Glu	Ile	Pro	Ile
	340							345					350		
Gly	Leu	Arg	Glu	Thr	Asp	Leu	Thr	Pro	Ala	His	Cys	His	Met	His	Thr
	355						360					365			
Asn	Pro	His	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Lys	Ser	Gly	Lys	Thr	Thr
	370						375					380			
Ile	Ala	His	Ala	Ile	Ala	Arg	Ala	Ile	Cys	Ala	Arg	Asn	Ser	Pro	Gln
385					390				395						400
Gln	Val	Arg	Phe	Met	Leu	Ala	Asp	Tyr	Arg	Ser	Gly	Leu	Leu	Asp	Ala
				405					410					415	
Val	Pro	Asp	Thr	His	Leu	Leu	Gly	Ala	Gly	Ala	Ile	Asn	Arg	Asn	Ser
				420				425					430		
Ala	Ser	Leu	Asp	Glu	Ala	Ala	Gln	Ala	Leu	Ala	Val	Asn	Leu	Lys	Lys
		435					440					445			
Arg	Leu	Pro	Pro	Thr	Asp	Leu	Thr	Thr	Ala	Gln	Leu	Arg	Ser	Arg	Ser
	450					455					460				
Trp	Trp	Ser	Gly	Phe	Asp	Val	Val	Leu	Leu	Val	Asp	Asp	Trp	His	Met
465					470					475					480
Ile	Val	Gly	Ala	Ala	Gly	Gly	Met	Pro	Pro	Met	Ala	Pro	Leu	Ala	Pro
				485				490						495	
Leu	Leu	Pro	Ala	Ala	Ala	Asp	Ile	Gly	Leu	His	Ile	Ile	Val	Thr	Cys
		500						505					510		
Gln	Met	Ser	Gln	Ala	Tyr	Lys	Ala	Thr	Met	Asp	Lys	Phe	Val	Gly	Ala
	515						520					525			
Ala	Phe	Gly	Ser	Gly	Ala	Pro	Thr	Met	Phe	Leu	Ser	Gly	Glu	Lys	Gln
	530					535					540				
Glu	Phe	Pro	Ser	Ser	Glu	Phe	Lys	Val	Lys	Arg	Arg	Pro	Pro	Gly	Gln
545					550				555						560
Ala	Phe	Leu	Val	Ser	Pro	Asp	Gly	Lys	Glu	Val	Ile	Gln	Ala	Pro	Tyr
				565				570						575	
Ile	Glu	Pro	Pro	Glu	Glu	Val	Phe	Ala	Ala	Pro	Pro	Ser	Ala	Gly	
		580					585						590		

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

191

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Asp Pro Val Asp Asp Ala Phe Ile Ala Lys Leu Asn Thr Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 14
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Asp Pro Val Asp Ala Ile Ile Asn Leu Asp Asn Tyr Gly Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 5
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Glu Met Lys Xaa Phe Lys Asn Ala Ile Val Gln Glu Ile Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

192

(ii) MOLECULE TYPE: None

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 3...3

(D) OTHER INFORMATION: Ala is Ala or Gln

(A) NAME/KEY: Other

(B) LOCATION: 7...7

(D) OTHER INFORMATION: Thr is Gly or Thr

(ix) Feature:

(A) NAME/KEY: Other

(B) LOCATION: 11

(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Val	Ile	Ala	Gly	Met	Val	Thr	His	Ile	His	Xaa	Val	Ala	Gly
1				5						10			

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr	Asn	Ile	Val	Val	Leu	Ile	Lys	Gln	Val	Pro	Asp	Thr	Trp	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala	Ile	Glu	Val	Ser	Val	Leu	Arg	Val	Phe	Thr	Asp	Ser	Asp	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 79:

193

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

- (ix) FEATURE:

- (A) NAME/KEY: Other
 (B) LOCATION: 4...4
 (D) OTHER INFORMATION: Asp is Asp or Glu

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Asp Pro Ala Asp Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
 1 5 10 15
 Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
 20 25 30
 Glu Ser Met Tyr Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr
 35 40 45
 Val Ser

50

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Thr	Thr	Ser	Pro	Asp	Pro	Tyr	Ala	Ala	Leu	Pro	Lys	Leu	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Thr	Glu	Tyr	Glu	Gly	Pro	Lys	Thr	Lys	Phe	His	Ala	Leu	Met	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Thr	Thr	Ile	Val	Ala	Leu	Lys	Tyr	Pro	Gly	Gly	Val	Val	Met	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

195

- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 15
- (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```
Ser Phe Pro Tyr Phe Ile Ser Pro Glu Xaa Ala Met Arg Glu Xaa
  1             5             10             15
```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
Thr His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr
  1             5             10             15
```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 107...450
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
AGCCCGGTAA TCGAGTTCGG GCAATGCTGA CCATCGGGTT TGTTCCTGGC TATAACCGAA      60
```

```
CGGTTTGTGT ACGGGATACA AATACAGGGA GGAAGAAGT AGGCAA ATG GAA AAA      115
```

```
Met Glu Lys
```

196

```

ATG TCA CAT GAT CCG ATC GCT GCC GAC ATT GGC ACG CAA GTG AGC GAC      163
Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln Val Ser Asp
      5              10              15

AAC GCT CTG CAC GGC GTG ACG GCC GGC TCG ACG GCG CTG ACG TCG GTG      211
Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu Thr Ser Val
      20              25              30              35

ACC GGG CTG GTT CCC GCG GGG GCC GAT GAG GTC TCC CCC CAA GCG GCG      259
Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala Gln Ala Ala
              40              45              50

ACG GCG TTC ACA TCG GAG GGC ATC CAA TTG CTG GCT TCC AAT GCA TCG      307
Thr Ala Phe Thr Ser Glu Gly Ile Gln Leu Leu Ala Ser Asn Ala Ser
              55              60              65

GCC CAA GAC CAG CTC CAC CGT GCG GGC GAA GCG GTC CAG GAC GTC GCC      355
Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln Asp Val Ala
              70              75              80

CGC ACC TAT TCG CAA ATC GAC GAC GCG GCC GCC GGC GTC TTC GCC TAATA      405
Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val Phe Ala
      85              90              95

GGCCCCCAAC ACATCGGAGG GAGTGATCAC CATGCTGTGG CACGC      450

```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

Met Glu Lys Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln
 1              5              10              15

Val Ser Asp Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu
      20              25              30

Thr Ser Val Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala
      35              40              45

Gln Ala Ala Thr Ala Phe Thr Ser Glu Gly Ile Gln Leu Leu Ala Ser
      50              55              60

Asn Ala Ser Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln
      65              70              75              80

Asp Val Ala Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val
      85              90              95

Phe Ala

```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...453
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GCAACCGGCT TTTCGATCAG CTGAGACATC ASCCGC GTG CGG GTC AAC GAC CCA	54
Met Arg Val Asn Asp Pro	
1 5	
CCT GCG CCA GGT AGC GAC TCC GCG CGC AGC AGG CCC GCG CCC GCG CTG	102
Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser Arg Pro Ala Pro Ala Leu	
10 15 20	
GGG CCT GAT CCA CCA GCC AGC GGA TGG TTC GAC AGC GGA CTG GTG CCG	150
Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe Asp Ser Gly Leu Val Pro	
25 30 35	
AGC AGG CCC ATC TGC GCG GCT TCC TCG TCG GCT GGG TTG CCG CCG CCG	198
Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser Ala Gly Leu Pro Pro Pro	
40 45 50	
GTG CCG CCC ACC TGG CTG AAC AAC GAC GTC ACC TGC TGC AGC GGC TGG	246
Val Pro Pro Thr Trp Leu Asn Asn Asp Val Thr Cys Cys Ser Gly Trp	
55 60 65 70	
GTC AGC TGC TGC ATC GGG CCG CTC ATC TCA CCC AGT TGG CCG AGG GTC	294
Val Ser Cys Cys Ile Gly Pro Leu Ile Ser Pro Ser Trp Pro Arg Val	
75 80 85	
TGG GTA GCC GCC GGC GGC AAC TGG CCA ACC GGT GTT GAG CTG CCA GGG	342
Trp Val Ala Ala Gly Gly Asn Trp Pro Thr Gly Val Glu Leu Pro Gly	
90 95 100	
GAG GGC ATT CCG AAG ATC GGG TTC GTC GTG CTC TGG CTC GCG CCG GGA	390
Glu Gly Ile Pro Lys Ile Gly Phe Val Val Leu Trp Leu Ala Pro Gly	
105 110 115	
TCA AGG ATC GAC GCC ATC GGC TCG AGC TTC TCG AAA AGC GTG TTA ACC	438
Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe Ser Lys Ser Val Leu Thr	
120 125 130	
GCG GTC TCG GCC TGG TAGACCT	460
Ala Val Ser Ala Trp	
135	

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

Met Arg Val Asn Asp Pro Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser
 1             5             10             15

Arg Pro Ala Pro Ala Leu Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe
          20             25             30

Asp Ser Gly Leu Val Pro Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser
          35             40             45

Ala Gly Leu Pro Pro Pro Val Pro Pro Thr Trp Leu Asn Asn Asp Val
 50             55             60

Thr Cys Cys Ser Gly Trp Val Ser Cys Cys Ile Gly Pro Leu Ile Ser
 65             70             75             80

Pro Ser Trp Pro Arg Val Trp Val Ala Ala Gly Gly Asn Trp Pro Thr
          85             90             95

Gly Val Glu Leu Pro Gly Glu Gly Ile Pro Lys Ile Gly Phe Val Val
          100            105            110

Leu Trp Leu Ala Pro Gly Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe
          115            120            125

Ser Lys Ser Val Leu Thr Ala Val Ser Ala Trp
          130            135

```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1140
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TAATAGGCCC CCAACACATC GGAGGGA GTG ATC ACC ATG CTG TGG CAC GCA ATG															54
Met Ile Thr Met Leu Trp His Ala Met															
1 5															
CCA CCG GAG CTA AAT ACC GCA CGG CTG ATG GCC GGC GCG GGT CCG GCT	102														
Pro Pro Glu Leu Asn Thr Ala Arg Leu Met Ala Gly Ala Gly Pro Ala															
10 15 20 25															
CCA ATG CTT GCG GCG GCC GCG GGA TGG CAG ACG CTT TCG GCG GCT CTG	130														
Pro Met Leu Ala Ala Ala Ala Gly Trp Gln Thr Leu Ser Ala Ala Leu															
30 35 40															
GAC GCT CAG GCC GTC GAG TTG ACC GCG CGC CTG AAC TCT CTG GGA GAA	198														
Asp Ala Gln Ala Val Glu Leu Thr Ala Arg Leu Asn Ser Leu Gly Glu															
45 50 55															
GCC TGG ACT GGA GGT GGC AGC GAC AAG GCG CTT GCG GCT GCA ACG CCG	246														
Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala Leu Ala Ala Ala Thr Pro															
60 65 70															
ATG GTG GTC TGG CTA CAA ACC GCG TCA ACA CAG GCC AAG ACC CGT GCG	294														
Met Val Val Trp Leu Gln Thr Ala Ser Thr Gln Ala Lys Thr Arg Ala															
75 80 85															
ATG CAG GCG ACG GCG CAA GCC GCG GCA TAC ACC CAG GCC ATG GCG ACG	342														
Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr Thr Gln Ala Met Ala Thr															
90 95 100 105															
ACG CCG TCG CTG CCG GAG ATC GCC GCC AAC CAC ATC ACC CAG GCC GTC	390														
Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn His Ile Thr Gln Ala Val															
110 115 120															
CTT ACG GCC ACC AAC TTC TTC GGT ATC AAC ACG ATC CCG ATC GCG TTG	438														
Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn Thr Ile Pro Ile Ala Leu															
125 130 135															
ACC GAG ATG GAT TAT TTC ATC CGT ADG TGG AAC CAG GCA GCC CTG GCA	486														
Thr Glu Met Asp Tyr Phe Ile Arg Met Trp Asn Gln Ala Ala Leu Ala															
140 145 150															
ATG GAG GTC TAC CAG GCC GAG ACC GCG GTT AAC ACG CTT TTC GAG AAG	534														
Met Glu Val Tyr Gln Ala Glu Thr Ala Val Asn Thr Leu Phe Glu Lys															
155 160 165															
CTC GAG CCG ATG GCG TCG ATC CTT GAT CCC GGC GCG AGC CAG AGC ACG	582														
Leu Glu Pro Met Ala Ser Ile Leu Asp Pro Gly Ala Ser Gln Ser Thr															
170 175 180 185															
ACG AAC CCG ATC TTC GGA ATG CCC TCC CCT GGC AGC TCA ACA CCG GTT	630														
Thr Asn Pro Ile Phe Gly Met Pro Ser Pro Gly Ser Ser Thr Pro Val															
190 195 200															
GCC CAG TTG CCG CCG GCG GCT ACC CAG ACC CTC GGC CAA CTG GGT GAG	678														
Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr Leu Gly Gln Leu Gly Glu															
205 210 215															
ATG ACC GGC CCG ATG CAG CAG CTG ACC CAG CCG CTG CAG CAG GTG ACG	726														
Met Ser Gly Pro Met Gln Gln Leu Thr Gln Pro Leu Gln Gln Val Thr															

200

220	225	230	
TCG TTG TTC AGC CAG GTG GGC GGC ACC GGC GGC GGC AAC CCA GCC GAC			774
Ser Leu Phe Ser Gln Val Gly Gly Thr Gly Gly Gly Asn Pro Ala Asp			
235	240	245	
GAG GAA GCC GCG CAG ATG GGC CTG CTC GGC ACC AGT CCG CTG TCG AAC			822
Glu Glu Ala Ala Gln Met Gly Leu Leu Gly Thr Ser Pro Leu Ser Asn			
250	255	260	265
CAT CCG CTG GCT GGT GGA TCA GGC CCC AGC GCG GGC GCG GGC CTG CTG			870
His Pro Leu Ala Gly Gly Ser Gly Pro Ser Ala Gly Ala Gly Leu Leu			
	270	275	280
CGC GCG GAG TCG CTA CCT GGC GCA GGT GGG TCG TTG ACC CGC ACG CCG			918
Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly Ser Leu Thr Arg Thr Pro			
	285	290	295
CTG ATG TCT CAG CTG ATC GAA AAG CCG GTT GCC CCC TCG GTG ATG CCG			966
Leu Met Ser Gln Leu Ile Glu Lys Pro Val Ala Pro Ser Val Met Pro			
	300	305	310
GCG GCT GCT GCC GGA TCG TCG GCG ACG GGT GGC GCC GCT CCG GTG GGT			1014
Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly Gly Ala Ala Pro Val Gly			
	315	320	325
GCG GGA GCG ATG GGC CAG GGT GCG CAA TCC GGC GGC TCC ACC AGC CCG			1062
Ala Gly Ala Met Gly Gln Gly Ala Gln Ser Gly Gly Ser Thr Arg Pro			
	330	335	340
GGT CTG GTC GCG CCG GCA CCG CTC GCG CAG GAG CGT GAA GAA GAC GAC			1110
Gly Leu Val Ala Pro Ala Pro Leu Ala Gln Glu Arg Glu Glu Asp Asp			
	350	355	360
GAG GAC GAC TGG GAC GAA GAG GAC GAC TGG TGAGCTCCCG TAATGACAAC AGA			1163
Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp			
	365	370	
CTTCCCGGCC ACCCGGGCCG GAGACTTGC CAACATT			1200

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Met	Ile	Thr	Met	Leu	Trp	His	Ala	Met	Pro	Pro	Glu	Leu	Asn	Thr	Ala
1				5					10					15	
Arg	Leu	Met	Ala	Gly	Ala	Gly	Pro	Ala	Pro	Met	Leu	Ala	Ala	Ala	Ala

201

20					25					30						
Gly	Trp	Gln	Thr	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu	
35					40					45						
Thr	Ala	Arg	Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser	
50					55					60						
Asp	Lys	Ala	Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr	
65					70					75					80	
Ala	Ser	Thr	Gln	Ala	Lys	Thr	Arg	Ala	Met	Gln	Ala	Thr	Ala	Gln	Ala	
85					90					95						
Ala	Ala	Tyr	Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile	
100					105					110						
Ala	Ala	Asn	His	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe	
115					120					125						
Gly	Ile	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Thr	Glu	Met	Asp	Tyr	Phe	Ile	
130					135					140						
Arg	Met	Trp	Asn	Gln	Ala	Ala	Leu	Ala	Met	Glu	Val	Tyr	Gln	Ala	Glu	
145					150					155					160	
Thr	Ala	Val	Asn	Thr	Leu	Phe	Glu	Lys	Leu	Glu	Pro	Met	Ala	Ser	Ile	
165					170					175						
Leu	Asp	Pro	Gly	Ala	Ser	Gln	Ser	Thr	Thr	Asn	Pro	Ile	Phe	Gly	Met	
180					185					190						
Pro	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Val	Gly	Gln	Leu	Pro	Pro	Ala	Ala	
195					200					205						
Thr	Gln	Thr	Leu	Gly	Gln	Leu	Gly	Glu	Met	Ser	Gly	Pro	Met	Gln	Gln	
210					215					220						
Leu	Thr	Gln	Pro	Leu	Gln	Gln	Val	Thr	Ser	Leu	Phe	Ser	Gln	Val	Gly	
225					230					235					240	
Gly	Thr	Gly	Gly	Gly	Asn	Pro	Ala	Asp	Glu	Glu	Ala	Ala	Gln	Met	Gly	
245					250					255						
Leu	Leu	Gly	Thr	Ser	Pro	Leu	Ser	Asn	His	Pro	Leu	Ala	Gly	Gly	Ser	
260					265					270						
Gly	Pro	Ser	Ala	Gly	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Ser	Leu	Pro	Gly	
275					280					285						
Ala	Gly	Gly	Ser	Leu	Thr	Arg	Thr	Pro	Leu	Met	Ser	Gln	Leu	Ile	Glu	
290					295					300						
Lys	Pro	Val	Ala	Pro	Ser	Val	Met	Pro	Ala	Ala	Ala	Ala	Gly	Ser	Ser	
305					310					315					320	
Ala	Thr	Gly	Gly	Ala	Ala	Pro	Val	Gly	Ala	Gly	Ala	Met	Gly	Gln	Gly	
325					330					335						

202

Ala Gln Ser Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro
 340 345 350

Leu Ala Gln Glu Arg Gln Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu
 355 360 365

Asp Asp Trp
 370

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...969
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GACGCGACAC	ASAAATCCTT	AAGGCCGGCG	GCCAGGGGGC	CGAAG	GTG	AAG	AAG	GTG	57							
								Met Lys Lys Val								
								1								
AAG	CCC	CAG	AAA	CCG	AAG	GCC	ACG	AAG	CCG	CCC	AAA	GTG	GTG	TCG	CAG	105
Lys	Pro	Gln	Lys	Pro	Lys	Ala	Thr	Lys	Pro	Pro	Lys	Val	Val	Ser	Gln	
5				10				15						20		
CGC	GGC	TGG	CGA	CAT	TGG	GTG	CAT	GCG	TTG	ACG	CGA	ATC	AAC	CTG	GGC	153
Arg	Gly	Trp	Arg	His	Trp	Val	His	Ala	Leu	Thr	Arg	Ile	Asn	Leu	Gly	
			25					30						35		
CTG	TCA	CCC	GAC	GAG	AAG	TAC	GAG	CTG	GAC	CTG	CAC	GCT	CGA	GTC	CGC	201
Leu	Ser	Pro	Asp	Glu	Lys	Tyr	Glu	Leu	Asp	Leu	His	Ala	Arg	Val	Arg	
			40				45						50			
CGC	AAT	CCC	CGC	GGG	TCG	TAT	CAG	ATC	GCC	GTC	GTC	GGT	CTC	AAA	GAT	249
Arg	Asn	Pro	Arg	Gly	Ser	Tyr	Gln	Ile	Ala	Val	Val	Gly	Leu	Lys	Gly	
	55					60						65				
GGG	GCT	GGC	AAA	ACC	ACG	CTG	ACA	GCA	GCG	TTG	GGG	TCG	ACG	TTG	GCT	297
Gly	Ala	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Leu	Gly	Ser	Thr	Leu	Ala	
70						75					80					
CAG	GTG	CGG	GCC	GAC	CSG	ATC	CTG	GCT	CTA	GAC	GCG	GAT	CCA	GCG	GCC	345
Gln	Val	Arg	Ala	Asp	Arg	Ile	Leu	Ala	Leu	Asp	Ala	Asp	Pro	Gly	Ala	
85					90				95					100		
GGA	AAC	CTC	GCC	GAT	CSG	GTA	GGG	CGA	CAA	TCG	GGC	GCG	ACC	ATC	GCT	393
Gly	Asn	Leu	Ala	Asp	Arg	Val	Gly	Arg	Gln	Ser	Gly	Ala	Thr	Ile	Ala	
			105				110						115			

203

GAT GTG CTT GCA GAA AAA GAG CTG TCG CAC TAC AAC GAC ATC CGC GCA	441
Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn Asp Ile Arg Ala	
120 125 130	
CAC ACT AGC GTC AAT GCG GTC AAT CTG GAA GTG CTG CCG GCA CCG GAA	489
His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu Pro Ala Pro Glu	
135 140 145	
TAC AGC TCG GCG CAG CGC GCG CTC AGC GAC GCC GAC TGG CAT TTC ATC	537
Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp Trp His Phe Ile	
150 155 160	
GCC GAT CCT GCG TCG AGG TTT TAC AAC CTC GTC TTG GCT GAT TGT GGG	585
Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly	
165 170 175 180	
GCC GGC TTC TTC GAC CCG CTG ACC CGC GGC GTG CTG TCC ACC GTG TCC	633
Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu Ser Thr Val Ser	
185 190 195	
GGT GTC GTG GTC GTG GCA AGT GTC TCA ATC GAC GGC GCA CAA CAG GCG	681
Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly Ala Gln Gln Ala	
200 205 210	
TCG GTC GCG TTG GAC TGG TTG CGC AAC AAC GGT TAC CAA GAT TTG GCG	729
Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala	
215 220 225	
AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT	777
Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn	
230 235 240	
GTC GCA GTT AAA GAC CTG GTG CCG CAT TTC GAA CAG CAA GTT CAA CCC	825
Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro	
245 250 255 260	
GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC	873
Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr	
265 270 275	
GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC	921
Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu	
280 285 290	
GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T	970
Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg	
295 300 305	
GAGCGCACCT GCTGTGCTG CTGGTCCTAC	1000

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

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Met Lys Lys Val Lys Pro Gln Lys Pro Lys Ala Thr Lys Pro Pro Lys
 1           5           10           15

Val Val Ser Gln Arg Gly Trp Arg His Trp Val His Ala Leu Thr Arg
      20           25           30

Ile Asn Leu Gly Leu Ser Pro Asp Glu Lys Tyr Glu Leu Asp Leu His
      35           40           45

Ala Arg Val Arg Arg Asn Pro Arg Gly Ser Tyr Gln Ile Ala Val Val
      50           55           60

Gly Leu Lys Gly Gly Ala Gly Lys Thr Thr Leu Thr Ala Ala Leu Gly
      65           70           75           80

Ser Thr Leu Ala Gln Val Arg Ala Asp Arg Ile Leu Ala Leu Asp Ala
      85           90           95

Asp Pro Gly Ala Gly Asn Leu Ala Asp Arg Val Gly Arg Gln Ser Gly
      100          105          110

Ala Thr Ile Ala Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn
      115          120          125

Asp Ile Arg Ala His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu
      130          135          140

Pro Ala Pro Glu Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp
      145          150          155          160

Trp His Phe Ile Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu
      165          170          175

Ala Asp Cys Gly Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu
      180          185          190

Ser Thr Val Ser Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly
      195          200          205

Ala Gln Gln Ala Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr
      210          215          220

Gln Asp Leu Ala Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro
      225          230          235          240

Gly Glu Pro Asn Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln
      245          250          255

Gln Val Gln Pro Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile
      260          265          270

Ala Ala Gly Thr Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys
      275          280          285

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